

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: PAUL, PREM S.
MENG, XIANG-JIN
HALBUR, PATRICK G.
MOROZOV, IGOR
LUM, MELISSA A.

(ii) TITLE OF INVENTION: A POLYNUCLEIC ACID ISOLATED FROM A PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS (PRRSV), A PROTEIN ENCODED BY THE POLYNUCLEIC ACID, A VACCINE PREPARED FROM OR CONTAINING THE POLYNUCLEIC ACID OR PROTEIN,

(iii) NUMBER OF SEQUENCES: 77

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Arlington
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/131,625
(B) FILING DATE: 05-OCT-1993

(viii) ATTORNEY/AGENT INFORMATION:

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(B) REGISTRATION NUMBER: 31,451
(C) REFERENCE/DOCKET NUMBER: 4625-021-55X CIP

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGCCGTGTG GTTCTCGCCA AT

22

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCCCATTTCCTCTAGCGAC TG

22

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCCGCGGAAC CATCAAGCAC

20

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAACTTGACG CTATGTGAGC

20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCGGTCTGGA TTGACGACAG

20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GACTGCTAGG GCTTCTGCAC

20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCCATTCAAGC TCACATAGCG

20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTCGTCAAGT ATGGCCGGT

19

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCCATTGCGC TGACTGTCA

19

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTGACGAGGA CTTCGGCTG

19

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCTCTACCTG CAATTCTGTG

20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GtgtatAGGA CCGGCAACCG

20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2062 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome
virus
(B) STRAIN: Iowa
(C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGCAGGGCTTT GCTGTCCTCC AAGACATCAG TTGCCTTAGG CATCGCAACT CGGCCTCTGA	60
GGCGATTTCGC AAAGTCCCTC AGTGCCGCAC GGCGATAGGG ACACCCGTGT ATATCACTGT	120
CACAGCCAAT GTTACCGATG AGAATTATTT GCATT CCTCT GATCTTCTCA TGCTTTCTTC	180
TTGCCTTTTC TATGCTTCTG AGATGAGTGA AAAGGGATT AAGGTGGTAT TTGGCAATGT	240
GTCAGGCATC GTGGCAGTGT GCGTCAACTT CACCAGTTAC GTCCAACATG TCAAGGAATT	300
TACCCAACGT TCCTTGGTAG TTGACCATGT GCGGCTGCTC CATTTCATGA CGCCCGAGAC	360
CATGAGGTGG GCAACTGTT TAGCCTGTCT TTTTGGCATT CTGTTGGCAA TTTGAATGTT	420
TAAGTATGTT GGGGAAATGC TTGACCGCGG GCTGTTGCTC GCAATTGCTT TTTTTGTGGT	480
GTATCGTGCC GTCTTGTCTT GTTGCCTCG TCAGCGCCAA CGGGAACAGC GGCTCAAATT	540
TACAGCTGAT TTACAACTTG ACGCTATGTG AGCTGAATGG CACAGATTGG CTAGCTAATA	600
AATTTGACTG GGCAGTGGAG TGTTTGTCAT TTTTCCTGT GTTGACTCAC ATTGTCTCTT	660
ATGGTGCCCT CACTACTAGC CATTCCCTTG ACACAGTCGG TCTGGTCACT GTGTCTACCG	720
CTGGGTTTGT TCACGGCGG TATGTTCTGA GTAGCATGTA CGCGGTCTGT GCCCTGGCTG	780
CGTTGATTG CTTCGTCATT AGGCTTGCAG AGAATTGCAT GTCCTGGCGC TACTCATGTA	840
CCAGATATAC CAACTTTCTT CTGGACACTA AGGGCAGACT CTATCGTTGG CGGTCGCCTG	900
TCATCATAGA GAAAAGGGGC AAAGTTGAGG TCGAAGGTCA CCTGATCGAC CTCAAAAGAG	960
TTGTGCTTGA TGGTTCCCGCG GCTACCCCTG TAACCAGAGT TTCAGCGGAA CAATGGAGTC	1020
GTCCTTAGAT GACTTCTGTC ATGATAGCAC GGCTCCACAA AAGGTGCTCT TGCGTTTTC	1080
TATTACCTAC ACGCCAGTGA TGATATATGC CCTAAAGGTG AGTCGCGGCC GACTGCTAGG	1140
GCTTCTGCAC CTTTTGGTCT TCCTGAATTG TGCTTCACC TTCGGGTACA TGACATTGCT	1200
GCACCTTCAG AGTACAAATA AGGTCGCGCT CACTATGGGA GCAGTAGTTG CACTCCTTTG	1260
GGGGGTGTAC TCAGCCATAG AAACCTGGAA ATTCACTCACC TCCAGATGCC GTTTGTGCTT	1320

GCTAGGCCGC AAGTACATTC TGGCCCTGCG ACCACACGTT GAAAGTGCCG CAGGCTTTCA	1380
TCCGATTGCG GCAAATGATA ACCACGCATT TGTCGTCCGG CGTCCCGGCT CCACTACGGT	1440
CAACGGCACA TTGGTGCCCCG GGTTAAAAG CCTCGTGTG GGTGGCAGAA AAGCTGTTAA	1500
ACAGGGAGTG GTAAACCTTG TTAAATATGC CAAATAACAC CGGCAAGCAG CAGAAGAGAA	1560
AGAAGGGGGA TGGCCAGCCA GTCAATCAGC TGTGCCAGAT GCTGGGTAAG ATCATCGCTC	1620
ACCAAAACCA GTCCAGAGGC AAGGGACCGG GAAAGAAAAA TAAGAAGAAA AACCCGGAGA	1680
AGCCCCATT CCCTCTAGCG ACTGAAGATG ATGTCAGACA TCACCTTACC CCTAGTGAGC	1740
GTCAATTGTG TCTGTCGTCA ATCCAGACCG CCTTTAATCA AGGCGCTGGG ACTTGCACCC	1800
TGTCAGATT AGGGAGGATA AGTTACACTG TGGAGTTAG TTTGCCTACG CATCATACTG	1860
TGCGCCTGAT CCGCGTCACA GCATCACCC CAGCATGATG GGCTGGCATT CTTGAGGCAT	1920
CCCAGTGTGTT GAATTGGAAG AATGCGTGGT GAATGGCACT GATTGACATT GTGCCTCTAA	1980
GTCACCTATT CAATTAGGGC GACCGTGTGG GGGTAAGATT TAATTGGCGA GAACCACACG	2040
GCCGAAATTAA AAAAAAAAAA AA	2062

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATG TTG GGG AAA TGC TTG ACC GCG GGC TGT TGC TCG CAA TTG CTT TTT	48
Met Leu Gly Lys Cys Leu Thr Ala Gly Cys Cys Ser Gln Leu Leu Phe	
1 5 10 15	

TTG TGG TGT ATC GTG CCG TCT TGT TTT GTT GCG CTC GTC AGC GCC AAC Leu Trp Cys Ile Val Pro Ser Cys Phe Val Ala Leu Val Ser Ala Asn	96
20 25 30	
GGG AAC AGC GGC TCA AAT TTA CAG CTG ATT TAC AAC TTG ACG CTA TGT Gly Asn Ser Gly Ser Asn Leu Gln Leu Ile Tyr Asn Leu Thr Leu Cys	144
35 40 45	
GAG CTG AAT GGC ACA GAT TGG CTA GCT AAT AAA TTT GAC TGG GCA GTG Glu Leu Asn Gly Thr Asp Trp Leu Ala Asn Lys Phe Asp Trp Ala Val	192
50 55 60	
GAG TGT TTT GTC ATT TTT CCT GTG TTG ACT CAC ATT GTC TCT TAT GGT Glu Cys Phe Val Ile Phe Pro Val Leu Thr His Ile Val Ser Tyr Gly	240
65 70 75 80	
GCC CTC ACT ACT AGC CAT TTC CTT GAC ACA GTC GGT CTG GTC ACT GTG Ala Leu Thr Thr Ser His Phe Leu Asp Thr Val Gly Leu Val Thr Val	288
85 90 95	
TCT ACC GCT GGG TTT GTT CAC GGG CGG TAT GTT CTG AGT AGC ATG TAC Ser Thr Ala Gly Phe Val His Gly Arg Tyr Val Leu Ser Ser Met Tyr	336
100 105 110	
GCG GTC TGT GCC CTG GCT GCG TTG ATT TGC TTC GTC ATT AGG CTT GCG Ala Val Cys Ala Leu Ala Leu Ile Cys Phe Val Ile Arg Leu Ala	384
115 120 125	
AAG AAT TGC ATG TCC TGG CGC TAC TCA TGT ACC AGA TAT ACC AAC TTT Lys Asn Cys Met Ser Trp Arg Tyr Ser Cys Thr Arg Tyr Thr Asn Phe	432
130 135 140	
CTT CTG GAC ACT AAG GGC AGA CTC TAT CGT TGG CGG TCG CCT GTC ATC Leu Leu Asp Thr Lys Gly Arg Leu Tyr Arg Trp Arg Ser Pro Val Ile	480
145 150 155 160	
ATA GAG AAA AGG GGC AAA GTT GAG GTC GAA GGT CAC CTG ATC GAC CTC Ile Glu Lys Arg Gly Lys Val Glu Val Glu Gly His Leu Ile Asp Leu	528
165 170 175	
AAA AGA GTT GTG CTT GAT GGT TCC GCG GCT ACC CCT GTA ACC AGA GTT Lys Arg Val Val Leu Asp Gly Ser Ala Ala Thr Pro Val Thr Arg Val	576
180 185 190	
TCA GCG GAA CAA TGG AGT CGT CCT TAG Ser Ala Glu Gln Trp Ser Arg Pro	603
195 200	

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Leu Gly Lys Cys Leu Thr Ala Gly Cys Cys Ser Gln Leu Leu Phe
1 5 10 15

Leu Trp Cys Ile Val Pro Ser Cys Phe Val Ala Leu Val Ser Ala Asn
20 25 30

Gly Asn Ser Gly Ser Asn Leu Gln Leu Ile Tyr Asn Leu Thr Leu Cys
35 40 45

Glu Leu Asn Gly Thr Asp Trp Leu Ala Asn Lys Phe Asp Trp Ala Val
50 55 60

Glu Cys Phe Val Ile Phe Pro Val Leu Thr His Ile Val Ser Tyr Gly
65 70 75 80

Ala Leu Thr Thr Ser His Phe Leu Asp Thr Val Gly Leu Val Thr Val
85 90 95

Ser Thr Ala Gly Phe Val His Gly Arg Tyr Val Leu Ser Ser Met Tyr
100 105 110

Ala Val Cys Ala Leu Ala Ala Leu Ile Cys Phe Val Ile Arg Leu Ala
115 120 125

Lys Asn Cys Met Ser Trp Arg Tyr Ser Cys Thr Arg Tyr Thr Asn Phe
130 135 140

Leu Leu Asp Thr Lys Gly Arg Leu Tyr Arg Trp Arg Ser Pro Val Ile
145 150 155 160

Ile Glu Lys Arg Gly Lys Val Glu Val Glu Gly His Leu Ile Asp Leu
165 170 175

Lys Arg Val Val Leu Asp Gly Ser Ala Ala Thr Pro Val Thr Arg Val
180 185 190

Ser Ala Glu Gln Trp Ser Arg Pro
195 200

(2) INFORMATION FOR SEO ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 525 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
 - ii) MOLECULE TYPE: cDNA
 - vi) ORIGINAL SOURCE:
 - (A) ORGANISM: porcine reproductive and respiratory syndrome virus
 - (B) STRAIN: Iowa
 - (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)
 - ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATG GAG TCG TCC TTA GAT GAC TTC TGT CAT GAT AGC ACG GCT CCA CAA Met Glu Ser Ser Leu Asp Asp Phe Cys His Asp Ser Thr Ala Pro Gln	48
1 5 10 15	
AAG GTG CTC TTG GCG TTT TCT ATT ACC TAC ACG CCA GTG ATG ATA TAT Lys Val Leu Leu Ala Phe Ser Ile Thr Tyr Thr Pro Val Met Ile Tyr	96
20 25 30	
GCC CTA AAG GTG AGT CGC GGC CGA CTG CTA GGG CTT CTG CAC CTT TTG Ala Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Leu Leu	144
35 40 45	
GTC TTC CTG AAT TGT GCT TTC ACC TTC GGG TAC ATG ACA TTC GTG CAC Val Phe Leu Asn Cys Ala Phe Thr Phe Gly Tyr Met Thr Phe Val His	192
50 55 60	
TTT CAG AGT ACA AAT AAG GTC GCG CTC ACT ATG GGA GCA GTA GTT GCA Phe Gln Ser Thr Asn Lys Val Ala Leu Thr Met Gly Ala Val Val Ala	240
65 70 75 80	
CTC CTT TGG GGG GTG TAC TCA GCC ATA GAA ACC TGG AAA TTC ATC ACC Leu Leu Trp Gly Val Tyr Ser Ala Ile Glu Thr Trp Lys Phe Ile Thr	288
85 90 95	
TCC AGA TGC CGT TTG TGC TTG CTA GGC CGC AAG TAC ATT CTG GCC CCT Ser Arg Cys Arg Leu Cys Leu Leu Gly Arg Lys Tyr Ile Leu Ala Pro	336
100 105 110	

GCC CAC CAC GTT GAA AGT GCC GCA GGC TTT CAT CCG ATT GCG GCA AAT Ala His His Val Glu Ser Ala Ala Gly Phe His Pro Ile Ala Ala Asn	384
115 120 125	
GAT AAC CAC GCA TTT GTC GTC CGG CGT CCC GGC TCC ACT ACG GTC AAC Asp Asn His Ala Phe Val Val Arg Arg Pro Gly Ser Thr Thr Val Asn	432
130 135 140	
GGC ACA TTG GTG CCC GGG TTA AAA AGC CTC GTG TTG GGT GGC AGA AAA Gly Thr Leu Val Pro Gly Leu Lys Ser Leu Val Leu Gly Gly Arg Lys	480
145 150 155 160	
GCT GTT AAA CAG GGA GTG GTA AAC CTT GTT AAA TAT GCC AAA Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys	522
165 170	
TAA	525

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 174 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Glu Ser Ser Leu Asp Asp Phe Cys His Asp Ser Thr Ala Pro Gln 1 5 10 15	
Lys Val Leu Leu Ala Phe Ser Ile Thr Tyr Thr Pro Val Met Ile Tyr 20 25 30	
Ala Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Leu Leu 35 40 45	
Val Phe Leu Asn Cys Ala Phe Thr Phe Gly Tyr Met Thr Phe Val His 50 55 60	
Phe Gln Ser Thr Asn Lys Val Ala Leu Thr Met Gly Ala Val Val Ala 65 70 75 80	
Leu Leu Trp Gly Val Tyr Ser Ala Ile Glu Thr Trp Lys Phe Ile Thr 85 90 95	
Ser Arg Cys Arg Leu Cys Leu Leu Gly Arg Lys Tyr Ile Leu Ala Pro 100 105 110	

Ala His His Val Glu Ser Ala Ala Gly Phe His Pro Ile Ala Ala Asn
115 120 125

Asp Asn His Ala Phe Val Val Arg Arg Pro Gly Ser Thr Thr Val Asn
130 135 140

Gly Thr Leu Val Pro Gly Leu Lys Ser Leu Val Leu Gly Gly Arg Lys
145 150 155 160

Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys
165 170

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATG CCA AAT AAC ACC GGC AAG CAG CAG AAG AGA AAG AAG GGG GAT GGC 48
Met Pro Asn Asn Thr Gly Lys Gln Gln Lys Arg Lys Lys Gly Asp Gly
1 5 10 15

CAG CCA GTC AAT CAG CTG TGC CAG ATG CTG GGT AAG ATC ATC GCT CAC 96
Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala His
20 25 30

CAA AAC CAG TCC AGA GGC AAG GGA CCG GGA AAG AAA AAT AAG AAG AAA 144
Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys Lys
35 40 45

AAC CCG GAG AAG CCC CAT TTC CCT CTA GCG ACT GAA GAT GAT GTC AGA 192
Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg
50 55 60

CAT CAC TTT ACC CCT AGT GAG CGT CAA TTG TGT CTG TCG TCA ATC CAG	240
His His Phe Thr Pro Ser Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln	
65 70 75 80	
ACC GCC TTT AAT CAA GGC GCT GGG ACT TGC ACC CTG TCA GAT TCA GGG	288
Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Thr Leu Ser Asp Ser Gly	
85 90 95	
AGG ATA AGT TAC ACT GTG GAG TTT AGT TTG CCT ACG CAT CAT ACT GTG	336
Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val	
100 105 110	
CGC CTG ATC CGC GTC ACA GCA TCA CCC TCA GCA TGA	372
Arg Leu Ile Arg Val Thr Ala Ser Pro Ser Ala	
115 120	

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Pro Asn Asn Thr Gly Lys Gln Gln Lys Arg Lys Lys Gly Asp Gly	
1 5 10 15	
Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala His	
20 25 30	
Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys Lys	
35 40 45	
Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg	
50 55 60	
His His Phe Thr Pro Ser Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln	
65 70 75 80	
Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Thr Leu Ser Asp Ser Gly	
85 90 95	
Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val	
100 105 110	
Arg Leu Ile Arg Val Thr Ala Ser Pro Ser Ala	
115 120	

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (C) INDIVIDUAL ISOLATE: Lelystad

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATG AGA TGT TCT CAC AAA TTG GGG CGT TTC TTG ACT CCG CAC TCT TGC Met Arg Cys Ser His Lys Leu Gly Arg Phe Leu Thr Pro His Ser Cys	48
1 5 10 15	
TTC TGG TGG CTT TTT TTG CTG TGT ACC GGC TTG TCC TGG TCC TTT GCC Phe Trp Trp Leu Phe Leu Leu Cys Thr Gly Leu Ser Trp Ser Phe Ala	96
20 25 30	
GAT GGC AAC GGC GAC AGC TCG ACA TAC CAA TAC ATA TAT AAC TTG ACG Asp Gly Asn Gly Asp Ser Ser Thr Tyr Gln Tyr Ile Tyr Asn Leu Thr	144
35 40 45	
ATA TGC GAG CTG AAT GGG ACC GAC TGG TTG TCC AGC CAT TTT GGT TGG Ile Cys Glu Leu Asn Gly Thr Asp Trp Leu Ser Ser His Phe Gly Trp	192
50 55 60	
GCA GTC GAG ACC TTT GTG CTT TAC CCG GTT GCC ACT CAT ATC CTC TCA Ala Val Glu Thr Phe Val Leu Tyr Pro Val Ala Thr His Ile Leu Ser	240
65 70 75 80	
CTG GGT TTT CTC ACA ACA AGC CAT TTT TTT GAC GCG CTC GGT CTC GGC Leu Gly Phe Leu Thr Thr Ser His Phe Phe Asp Ala Leu Gly Leu Gly	288
85 90 95	
GCT GTA TCC ACT GCA GGA TTT GTT GGC GGG CGG TAC GTA CTC TGC AGC Ala Val Ser Thr Ala Gly Phe Val Gly Gly Arg Tyr Val Leu Cys Ser	336
100 105 110	

GTC TAC GGC GCT TGT GCT TTC GCA GCG TTC GTA TGT TTT GTC ATC CGT Val Tyr Gly Ala Cys Ala Phe Ala Ala Phe Val Cys Phe Val Ile Arg	384
115 120 125	
 GCT GCT AAA AAT TGC ATG GCC TGC CGC TAT GCC CGT ACC CGG TTT ACC Ala Ala Lys Asn Cys Met Ala Cys Arg Tyr Ala Arg Thr Arg Phe Thr	432
130 135 140	
 AAC TTC ATT GTG GAC GAC CGG GGG AGA GTT CAT CGA TGG AAG TCT CCA Asn Phe Ile Val Asp Asp Arg Gly Arg Val His Arg Trp Lys Ser Pro	480
145 150 155 160	
 ATA GTG GTA GAA AAA TTG GGC AAA GCC GAA GTC GAT GGC AAC CTC GTC Ile Val Val Glu Lys Leu Gly Lys Ala Glu Val Asp Gly Asn Leu Val	528
165 170 175	
 ACC ATC AAA CAT GTC GTC CTC GAA GGG GTT AAA GCT CAA CCC TTG ACG Thr Ile Lys His Val Val Leu Glu Gly Val Lys Ala Gln Pro Leu Thr	576
180 185 190	
 AGG ACT TCG GCT GAG CAA TGG GAG GCC TAG Arg Thr Ser Ala Glu Gln Trp Glu Ala	606
195 200	

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - ii) MOLECULE TYPE: protein
 - xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

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Met Arg Cys Ser His Lys Leu Gly Arg Phe Leu Thr Pro His Ser Cys
   1           5           .          10          .          15

Phe Trp Trp Leu Phe Leu Leu Cys Thr Gly Leu Ser Trp Ser Phe Ala
   20          .          25          .          30          .

Asp Gly Asn Gly Asp Ser Ser Thr Tyr Gln Tyr Ile Tyr Asn Leu Thr
   35          .          40          .          45          .

Ile Cys Glu Leu Asn Gly Thr Asp Trp Leu Ser Ser His Phe Gly Trp
   50          .          55          .          60          .

Ala Val Glu Thr Phe Val Leu Tyr Pro Val Ala Thr His Ile Leu Ser
   65          .          70          .          75          .          80

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Leu Gly Phe Leu Thr Thr Ser His Phe Phe Asp Ala Leu Gly Leu Gly
85 90 95

Ala Val Ser Thr Ala Gly Phe Val Gly Gly Arg Tyr Val Leu Cys Ser
100 105 110

Val Tyr Gly Ala Cys Ala Phe Ala Ala Phe Val Cys Phe Val Ile Arg
115 120 125

Ala Ala Lys Asn Cys Met Ala Cys Arg Tyr Ala Arg Thr Arg Phe Thr
130 135 140

Asn Phe Ile Val Asp Asp Arg Gly Arg Val His Arg Trp Lys Ser Pro
145 150 155 160

Ile Val Val Glu Lys Leu Gly Lys Ala Glu Val Asp Gly Asn Leu Val
165 170 175

Thr Ile Lys His Val Val Leu Glu Gly Val Lys Ala Gln Pro Leu Thr
180 185 190

Arg Thr Ser Ala Glu Gln Trp Glu Ala
195 200

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TGGGCTGGCA TTCTTGAGGC ATCCCAGTGT TTGAATTGGA AGAATGCGTG GTGAATGGCA 60
CTGATTGACA TTGTGCCTCT AAGTCACCTA TTCAATTAGG GCGACCGTGT GGGGGTAAGA 120
TTTAATTGGC GAGAACCCACA CGGCCGAAAT TAAAAAAA AAAA 164

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (C) INDIVIDUAL ISOLATE: Lelystad

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATG GGA GGC CTA GAC GAT TTT TGC AAC GAT CCT ATC GCC GCA CAA AAG Met Gly Gly Leu Asp Asp Phe Cys Asn Asp Pro Ile Ala Ala Gln Lys	48
1 5 10 15	
CTC GTG CTA GCC TTT AGC ATC ACA TAC ACA CCT ATA ATG ATA TAC GCC Leu Val Leu Ala Phe Ser Ile Thr Tyr Thr Pro Ile Met Ile Tyr Ala	96
20 25 30	
CTT AAG GTG TCA CGC GGC CGA CTC CTG GGG CTG TTG CAC ATC CTA ATA Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Ile Leu Ile	144
35 40 45	
TTT CTG AAC TGT TCC TTT ACA TTC GGA TAC ATG ACA TAT GTG CAT TTT Phe Leu Asn Cys Ser Phe Thr Phe Gly Tyr Met Thr Tyr Val His Phe	192
50 55 60	
CAA TCC ACC AAC CGT GTC GCA CTT ACC CTG GGG GCT GTT GTC GCC CTT Gln Ser Thr Asn Arg Val Ala Leu Thr Leu Gly Ala Val Val Ala Leu	240
65 70 75 80	
CTG TGG GGT GTT TAC AGC TTC ACA GAG TCA TGG AAG TTT ATC ACT TCC Leu Trp Gly Val Tyr Ser Phe Thr Glu Ser Trp Lys Phe Ile Thr Ser	288
85 90 95	
AGA TGC AGA TTG TGT TGC CTT GGC CGG CGA TAC ATT CTG GCC CCT GCC Arg Cys Arg Leu Cys Cys Leu Gly Arg Arg Tyr Ile Leu Ala Pro Ala	336
100 105 110	

CAT CAC GTA GAA AGT GCT GCA GGT CTC CAT TCA ATC TCA GCG TCT GGT	384
His His Val Glu Ser Ala Ala Gly Leu His Ser Ile Ser Ala Ser Gly	
115 120 125	
AAC CGA GCA TAC GCT GTG AGA AAG CCC GGA CTA ACA TCA GTG AAC GGC	432
Asn Arg Ala Tyr Ala Val Arg Lys Pro Gly Leu Thr Ser Val Asn Gly	
130 135 140	
ACT CTA GTA CCA GGA CTT CGG AGC CTC GTG CTG GGC GGC AAA CGA GCT	480
Thr Leu Val Pro Gly Leu Arg Ser Leu Val Leu Gly Gly Lys Arg Ala	
145 150 155 160	
GTT AAA CGA GGA GTG GTT AAC CTC GTC AAG TAT GGC CGG TAA	522
Val Lys Arg Gly Val Val Asn Leu Val Lys Tyr Gly Arg	
165 170	

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 173 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Gly Gly Leu Asp Asp Phe Cys Asn Asp Pro Ile Ala Ala Gln Lys	
1 5 10 15	
Leu Val Leu Ala Phe Ser Ile Thr Tyr Thr Pro Ile Met Ile Tyr Ala	
20 25 30	
Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Ile Leu Ile	
35 40 45	
Phe Leu Asn Cys Ser Phe Thr Phe Gly Tyr Met Thr Tyr Val His Phe	
50 55 60	
Gln Ser Thr Asn Arg Val Ala Leu Thr Leu Gly Ala Val Val Ala Leu	
65 70 75 80	
Leu Trp Gly Val Tyr Ser Phe Thr Glu Ser Trp Lys Phe Ile Thr Ser	
85 90 95	
Arg Cys Arg Leu Cys Cys Leu Gly Arg Arg Tyr Ile Leu Ala Pro Ala	
100 105 110	
His His Val Glu Ser Ala Ala Gly Leu His Ser Ile Ser Ala Ser Gly	
115 120 125	

Asn Arg Ala Tyr Ala Val Arg Lys Pro Gly Leu Thr Ser Val Asn Gly
130 135 140

Thr Leu Val Pro Gly Leu Arg Ser Leu Val Leu Gly Gly Lys Arg Ala
145 150 155 160

Val Lys Arg Gly Val Val Asn Leu Val Lys Tyr Gly Arg
165 170

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (C) INDIVIDUAL ISOLATE: Lelystad

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATG GCC GGT AAA AAC CAG AGC CAG AAG AAA AAG AAA AGT ACA GCT CCG	48
Met Ala Gly Lys Asn Gln Ser Gln Lys Lys Lys Ser Thr Ala Pro	
1 5 10 15	
ATG GGG AAT GGC CAG CCA GTC AAT CAA CTG TGC CAG TTG CTG GGT GCA	96
Met Gly Asn Gly Gln Pro Val Asn Gln Leu Cys Gln Leu Leu Gly Ala	
20 25 30	
ATG ATA AAG TCC CAG CGC CAG CAA CCT AGG GGA GGA CAG GCC AAA AAG	144
Met Ile Lys Ser Gln Arg Gln Gln Pro Arg Gly Gly Gln Ala Lys Lys	
35 40 45	
AAA AAG CCT GAG AAG CCA CAT TTT CCC CTG GCT GCT GAA GAT GAC ATC	192
Lys Lys Pro Glu Lys Pro His Phe Pro Leu Ala Ala Glu Asp Asp Ile	
50 55 60	
CGG CAC CAC CTC ACC CAG ACT GAA CGC TCC CTC TGC TTG CAA TCG ATC	240
Arg His His Leu Thr Gln Thr Glu Arg Ser Leu Cys Leu Gln Ser Ile	
65 70 75 80	

CAG ACG GCT TTC AAT CAA GGC GCA GGA ACT GCG TCG CTT TCA TCC AGC Gln Thr Ala Phe Asn Gln Gly Ala Gly Thr Ala Ser Leu Ser Ser Ser	288
85 90 95	
GGG AAG GTC AGT TTT CAG GTT GAG TTT ATG CTG CCG GTT GCT CAT ACA Gly Lys Val Ser Phe Gln Val Glu Phe Met Leu Pro Val Ala His Thr	336
100 105 110	
GTG CGC CTG ATT CGC GTG ACT TCT ACA TCC GCC AGT CAG GGT GCA AGT Val Arg Leu Ile Arg Val Thr Ser Thr Ser Ala Ser Gln Gly Ala Ser	384
115 120 125	
TAA	387

(2) INFORMATION FOR SEO ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 128 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - ii) MOLECULE TYPE: protein
 - xi) SEQUENCE DESCRIPTION: SEQ ID N

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Met Ala Gly Lys Asn Gln Ser Gln Lys Lys Lys Ser Thr Ala Pro
   1           5           10          15

Met Gly Asn Gly Gln Pro Val Asn Gln Leu Cys Gln Leu Leu Gly Ala
   20          25           30

Met Ile Lys Ser Gln Arg Gln Gln Pro Arg Gly Gly Gln Ala Lys Lys
   35          40           45

Lys Lys Pro Glu Lys Pro His Phe Pro Leu Ala Ala Glu Asp Asp Ile
   50          55           60

Arg His His Leu Thr Gln Thr Glu Arg Ser Leu Cys Leu Gln Ser Ile
   65          70           75           80

Gln Thr Ala Phe Asn Gln Gly Ala Gly Thr Ala Ser Leu Ser Ser Ser
   85          90           95

Gly Lys Val Ser Phe Gln Val Glu Phe Met Leu Pro Val Ala His Thr
  100         105          110

Val Arg Leu Ile Arg Val Thr Ser Thr Ser Ala Ser Gln Gly Ala Ser
  115         120          125

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(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (C) INDIVIDUAL ISOLATE: Lelystad

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TTTGACAGTC AGGTGAATGG CCGCGATTGG CGTGTGGCCT CTGAGTCACC TATTCAATTA	60
GGGCGATCAC ATGGGGGTCA TACTTAATCA GGCAGGAACC ATGTGACCGA AATTAAAAAA	120
AAAAAAA	127

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGGGATCCGG TATTGGCAA TGTGTC	26
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(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGTGTTCACGAGAACCG CTTAAGGG

28

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GGGGATCCAG AGTTTCAGCG G

21

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CAGTTAGTCG ACACGGTCTT AAGGG

25

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GGGGATCCTT GTTAAATATG CC

22

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTTACGCACC ACTTAAGGG

19

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AATGGGGCTT CTCCGG

16

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 886 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATGGAGTCGT CCTTAGATGA CTTCTGTCAT GATAGCACGG CTCCACAAAA GGTGCTTTG	60
GCGTTTCTA TTACCTACAC GCCAGTGATG ATATATGCCC TAAAGGTGAG TCGCGGCCGA	120
CTGCTAGGGC TTCTGCACCT TTTGGTCTTC CTGAATTGTG CTTTCACCTT CGGGTACATG	180
ACATTCGTGC ACTTTCAGAG TACAAATAAG GTCGCGCTCA CTATGGAGC AGTAGTTGCA	240
CTCCTTGGG GGGTGTACTC AGCCATAGAA ACCTGGAAAT TCATCACCTC CAGATGCCGT	300
TTGTGCTTGC TAGGCCGCAA GTACATTCTG GCCCCTGCC ACCACGTTGA AAGTGCCGCA	360
GGCTTCATC CGATTGCGGC AAATGATAAC CACGCATTTG TCGTCCGGCG TCCCGGCTCC	420
ACTACGGTCA ACGGCACATT GGTGCCCGGG TTAAAAAGCC TCGTGTGAGG TGGCAGAAAA	480
GCTGTTAAC AGGGAGTGGT AACACTTGTT AAATATGCCA ATAACACCG GCAAGCAGCA	540
GAAGAGAAAG AAGGGGGATG GCCAGCCAGT CAATCAGCTG TGCCAGATGC TGGGTAAGAT	600
CATCGCTCAC CAAAACCAGT CCAGAGGCAA GGGACCGGA AAGAAAAATA AGAAGAAAAA	660
CCCGGAGAAG CCCCATTTCC CTCTAGCGAC TGAAGATGAT GTCAGACATC ACTTTACCCC	720
TAGTGAGCGT CAATTGTGTC TGTGTCAT CCAGACCGCC TTTAATCAAG GCGCTGGAC	780
TTGCACCCCTG TCAGATTCAAG GGAGGATAAG TTACACTGTG GAGTTAGTT TGCCTACGCA	840
TCATACTGTG CGCCTGATCC GCGTCACAGC ATCACCCCTCA GCATGA	886

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 886 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-1894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ATGGGGTCGT CCTTAGATGA CTTCTGCCAT GATAGTACGG CTCCACAAAA GGTGCTTTG	60
GCGTTTCTA TTACCTACAC GCCAGTGATG ATATATGCCC TAAAGGTGAG TCGCGGCCGA	120
CTGCTAGGGC TTCTGCACCT TTTGATCTTC CTGAATTGTG CTTTCACCTT CGGGTACATG	180
ACATTCGTGC ACTTTCAGAG TACAAATAAG GTCGCGCTCA CTATGGGAGC AGTAGTTGCA	240
CTCCTTGGG GGGTGTACTC AGCCATAGAA ACCTGGAAAT TCATCACCTC CAGATGCCGT	300
TTGTGCTTGC TAGGCCGCAA GTACATTCTG GCCCCTGCC ACCACGTTGA AAGTGCCGCA	360
GGCTTTCATC CGATTGCGGC AAATGATAAC CACGCATTG TCGTCCGGCG TCCCGGCTCC	420
ACTACGGTCA ACGGCACATT GGTGCCCGGG TTGAAAAGCC TCGTGTGTTGGG TGGCAGAAAA	480
GCTGTTAAC AGGGAGTGGT AAACCTTGTC AAATATGCCA AATAACAACG GCAAGCAGCA	540
GAAGAGAAAG AAGGGGGATG GCCAGCCAGT CAATCAGCTG TGCCAGATGC TGGGTAAGAT	600
CATCGCTCAG CAAAACCAGT CCAGAGGCAA GGGACCGGGA AAGAAAAACA AGAAGAAAAAA	660
CCCGGAGAAG CCCCATTTC CTCTAGCGAC TGAAGATGAT GTCAGACATC ACTTCACCCC	720
TAGTGAGCGG CAATTGTGTC TGTCGTCAAT CCAGACCGCC TTTAATCAAG GCGCTGGGAC	780
TTGCACCCCTG TCAGATTCAAG GGAGGATAAG TTACACTGTG GAGTTAGTT TGCCAACGCA	840
TCATACTGTG CGCTTGATCC GCGTCACAGC ATCACCCCTCA GCATGA	886

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 886 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-22 (VR 2429)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATGGGGTCGT CCTTAGATGA CTTCTGTCAT GACAGCACGG CTCCACAAAA GGTGCTTTG	60
GCGTTTCTA TTACCTACAC GCCAGTGATG ATATATGCCC TGAAGGTGAG TCGCGGCCGA	120
CTGCTAGGGC TTCTGCACCT TTTGATCTTC CTGAATTGTG CTTTCACCTT CGGGTACATG	180
ACATTCGTGC ACTTTCAGAG TACAAATAAG GTCGCACTCA CTATGGGAGC AGTAGTTGCA	240
CTCCTTGGA GGGTGTACTC AGCCATAGAA ACCTGGAAAT TCATCACCTC CAGATGCCGT	300
TTGTGCTTGC TAGGCCGCAA GTACATTCTG GCCCCTGCC ACCACGTTGA AAGTGCCGCA	360
GGCTTTCATC CGATTGCGGC AAATGATAAC CACGCATTG TCGTTCGCGC TCCCGGCTCC	420
ACTACGGTCA ACGGCACATT GGTGCCCGGG TTGAAAAGCC TCGTGTGTTGGG TGGCAGAAAA	480
GCTGTTAACAC AGGGAGTGGT AAACCTTGTCA AAATATGCCA ATAACAACG GTAAGCAGCA	540
GAAGAGAAAG AAGGGGGATG GCCAGCCAGT CAATCAGCTG TGCCAGATGC TGGGCAAGAT	600
CATCGCTCAG CAAAATCAGT CCAGAGGCAA GGGACCGGGA AAGAAAATA AGAAGAAAAA	660
CCCGGAGAAG CCCCATTTTC CTCTAGCGAC TGAAGATGAT GTCAGACATC ACTTTACCCC	720
TAGTGAGCGG CAATTGTGTC TGCGTCAAT CCAGACCGCC TTTAATCAAG GCGCTGGGAC	780
TTGCACCCCTG TCAGATTCAAG GGAGGATAAG TTACACTGTG GAGTTTAGTT TGCCTACGCA	840
TCATACTGTG CGCCTGATCC GCGTCACAGC ATCACCCCTCA GCATGA	886

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 886 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATGGGGTCGT CCTTAGATGA CTTCTGTTAT GATA GTACGG CTCCACAAAA GGTGCTTTG	60
GCATTTCTA TTACCTACAC GCCAGTAATG ATATATGCCC TAAAGGTGAG TCGCGGCCGA	120
CTGCTAGGGC TTCTGCACCT TTTGATTTC CTGAACGTGTG CTTTCACCTT CGGGTACATG	180
ACATTCAATGC ACTTTCAGAG TACAAATAAG GTCGCGCTCA CTATGGGAGC AGTAGTTGCA	240
CTCCTTGGA GGGTGTACTC AGCCATAGAA ACCTGGAAAT TCATCACCTC CAGATGCCGT	300
TTGTGCTTGC TAGGCCGCAA GTACATTCTG GCCCCTGCC ACCACGTTGA AAGTGCCGCA	360
GGCTTCATC CGATTGCGGC AAATGATAAC CACGCATTG TCGTCCGGCG TCCCGGCTCC	420
ACTACGGTCA ACGGCACATT GGTGCCCGGG TTGAAAAGCC TCGTGTGTTGGG TGGCAGAAAA	480
GCTGTTAACAC AGGGAGTGGT AAACCTTGTC AAATATGCCA ATAACAACG GCAAGCAGCA	540
GAAGAGAAAG AAGGGGGATG GCCAGCCAGT CAATCAGCTG TGCCAGATGC TGGGTAAGAT	600
CATCGCCCAG CAAAACCAGT CTAGAGGCAA GGGACCGGGA AAGAAAATA AGAAGAAAAA	660
CCCGGAGAAG CCCCATTTTC CTCTAGCGAC TGAAGATGAT GTCAGACATC ACTTTACCCC	720
TAGTGAGCGG CAATTGTGTC TGTCGTCAAT CCAAACGTGCC TTTAATCAAG GCGCTGGGAC	780
TTGCACCCCTG TCAGATTCAAG GGAGGATAAG TTACACTGTG GAGTTTAGTT TGCCTACGCA	840
TCATACTGTG CGCTTGATCC GCGTCACAGC ATCACCCCTCA GCATGA	886

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 886 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-55 (VR 2430)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATGGGGTCGT CCTTAGATGA CTTCTGCCAT GATAGCACGG CTCCACAAAA GGTGCTTTG	60
GCGTTCTCTA TTACCTACAC GCCAGTGATG ATATATGCCC TAAAAGTAAG TCGCGGCCGA	120
CTGCTAGGGC TTCTGCACCT TTTGATCTTC CTAAATTGTG CTTTCACCTT CGGGTACATG	180
ACATTCGTGC ACTTTCAGAG CACAAACAAG GTCGCGCTCA CTATGGGAGC AGTAGTTGCA	240
CTCCTTGCG GGGTGTACTC AGCCATAGAA ACCTGGAAAT TCATCACCTC CAGATGCCGT	300
TTGTGCTTGC TAGGCCGCAA GTACATTTG GCCCCTGCC ACCACGTTGA AAGTGCCGCA	360
GGCTTTCATC CGATAGCGGC AAATGATAAC CACGCATTTG TCGTCCGGCG TCCCGGCTCC	420
ACTACGGTTA ACGGCACATT GGTGCCCGGG TTGAAAAGCC TCGTGTGTTGGG TGGCAGAAAA	480
GCTGTCAAAC AGGGAGTGGT AACACTTGTT AAATATGCCA AATAACAACG GCAAGCAGCA	540
GAAGAAAAAG AAGGGGGATG GCCAGCCAGT CAATCAGCTG TGCCAGATGC TGGGTAAGAT	600
CATCGCTCAG CAAAACCACT CCAGAGGCAA GGGACCGGGA AAGAAAAACA AGAAGAAAAA	660
CCC GGAGAAG CCCCATTTTC CTCTAGCGAC TGAAGATGAT GTCAGACATC ACTTCACCTC	720
TGGTGAGCGG CAATTGTGTC TGTCGTCAAT CCAGACAGCC TTTAATCAAG GCGCTGGAAC	780
TTGTACCCCTG TCAGATTCAAG GGAGGATAAG TTACACTGTG GAGTTTAGTT TGCCGACGCA	840
TCATACTGTG CGCTTGATCC GCGTCACAGC GTCACCCCTCA GCATGA	886

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 886 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-3927 (VR 2431)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATGGGGTCGT CCCTAGACGA CTTTGCAAT GATAGCACGG CTCCACAAAA GGTGCTTTG	60
GCGTTTCTA TTACCTACAC GCCGGTGATG ATATATGCTC TAAAGGTAAG TCGCGGCCGA	120
CTGCTAGGGC TTCTGCACCT TTTGATTCTT CTGAATTGTG CTTTACTTT CGGGTACATG	180
ACATTCGTGC ACTTGAGAG CACAAATAGG GTCGCGCTCA CTATGGGAGC AGTAGTCGCA	240
CTTCTCTGGG GGGTGTACTC AGCCATAGAA ACCTGGAAAT TCATCACCTC CAGATGCCGT	300
TTGTGCTTGC TAGGCCGCAA GTACATTCTG GCCCCTGCC ACCACGTTGA GAGTGCCGCA	360
GGCTTCATC CGATTGCGGC AAATGATAAC CACGCATTG TCGTCCGGCG TCCCGGCTCC	420
ACTACGGTTA ACGGCACATT GGTGCCCGGG TTGAGAAGCC TCGTGTGTTGGG TGGCAAAAAA	480
GCTGTTAACG AGGGAGTGGT AACACCTTGT AAATATGCCA ATAACAACG GCAAGCAGCA	540
GAAGAAAAAG AAGGGGGATG GCCAGCCAGT CAATCAGCTC TGCCAAATGC TGGGTAAGAT	600
CATCGCCCAG CAAAACCACT CCAGAGGTAA GGGACCGGGA AAGAAAAATA AGAAGAAAAA	660
CCCGGAGAAG CCCCATTTTC CTCTAGCGAC TGAAGATGAT GTCAGACATC ACTTCACCCCC	720
CAGTGAGCGG CAATTGTGTC TGTCGTCAAT CCAGACTGCC TTTAATCAGG GCGCTGGGAC	780
CTGTATCCTA TCAGATTCAAG GGAGGATAAG TTACACTGTG GAGTTAGTT TGCCGACGCA	840
TCATACTGTG CGCCTGATTC GCGTCACGGC ACCACCCTCA GCATGA	886

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 898 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (C) INDIVIDUAL ISOLATE: Lelystad

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ATGGGAGGCC TAGACGATT TTGCAACGAT CCTATGCCG CACAAAAGCT CGTGCTAGCC	60
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TTTACGCATCA CATAACACACC TATAATGATA TACGCCCTTA AGGTGTCACG CGGCCGACTC	120
CTGGGGCTGT TGCACATCCT AATATTCTG AACTGTCCT TTACATTGG ATACATGACA	180
TATGTGCATT TTCAATCCAC CAACCGTGT GCACTTACCC TGGGGGCTGT TGTCGCCCTT	240
CTGTGGGTG TTTACAGCTT CACAGAGTCA TGGAAGTTA TCACTTCCAG ATGCAGATTG	300
TGTTGCCTTG GCCGGCGATA CATTCTGGCC CCTGCCCATC ACGTAGAAAG TGCTGCAGGT	360
CTCCATTCAA TCTCAGCGTC TGGTAACCGA GCATACGCTG TGAGAAAGCC CGGACTAAC	420
TCAGTGAACG GCACTCTAGT ACCAGGACTT CGGAGCCTCG TGCTGGCGG CAAACGAGCT	480
GTTAACGAG GAGTGGTTAA CCTCGTCAAG TATGGCCGGT AAAAACAGA GCCAGAAGAA	540
AAAGAAAAGT ACAGCTCCGA TGGGAATGG CCAGCCAGTC AATCAACTGT GCCAGTTGCT	600
GGGTGCAATG ATAAAGTCCC AGGCCAGCA ACCTAGGGGA GGACAGGCCA AAAAGAAAAA	660
GCCTGAGAAG CCACATTTTC CCCTGGCTGC TGAAGATGAC ATCCGGCACC ACCTCACCCA	720
GACTGAACGC TCCCTCTGCT TGCAATCGAT CCAGACGGCT TTCAATCAAG GCGCAGGAAC	780
TGCGTCGCTT TCATCCAGCG GGAAGGTCAG TTTTCAGGTT GAGTTATGC TGCCGGTTGC	840
TCATACAGTG CGCCTGATTC GCGTGAATTAC TACATCCGCC AGTCAGGGTG CAAGTTAA	898

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-1894

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ATG GGG TCG TCC TTA GAT GAC TTC TGC CAT GAT AGT ACG GCT CCA CAA Met Gly Ser Ser Leu Asp Asp Phe Cys His Asp Ser Thr Ala Pro Gln 1 5 10 15	48
AAG GTG CTT TTG GCG TTT TCT ATT ACC TAC ACG CCA GTG ATG ATA TAT Lys Val Leu Leu Ala Phe Ser Ile Thr Tyr Thr Pro Val Met Ile Tyr 20 25 30	96
GCC CTA AAG GTG AGT CGC GGC CGA CTG CTA GGG CTT CTG CAC CTT TTG Ala Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Leu Leu 35 40 45	144
ATC TTC CTG AAT TGT GCT TTC ACC TTC GGG TAC ATG ACA TTC GTG CAC Ile Phe Leu Asn Cys Ala Phe Thr Phe Gly Tyr Met Thr Phe Val His 50 55 60	192
TTT CAG AGT ACA AAT AAG GTC GCG CTC ACT ATG GGA GCA GTA GTT GCA Phe Gln Ser Thr Asn Lys Val Ala Leu Thr Met Gly Ala Val Val Ala 65 70 75 80	240
CTC CTT TGG GGG GTG TAC TCA GCC ATA GAA ACC TGG AAA TTC ATC ACC Leu Leu Trp Gly Val Tyr Ser Ala Ile Glu Thr Trp Lys Phe Ile Thr 85 90 95	288
TCC AGA TGC CGT TTG TGC TTG CTA GGC CGC AAG TAC ATT CTG GCC CCT Ser Arg Cys Arg Leu Cys Leu Leu Gly Arg Lys Tyr Ile Leu Ala Pro 100 105 110	336
GCC CAC CAC GTT GAA AGT GCC GCA GGC TTT CAT CCG ATT GCG GCA AAT Ala His His Val Glu Ser Ala Ala Gly Phe His Pro Ile Ala Ala Asn 115 120 125	384
GAT AAC CAC GCA TTT GTC GTC CGG CGT CCC GGC TCC ACT ACG GTC AAC Asp Asn His Ala Phe Val Val Arg Arg Pro Gly Ser Thr Thr Val Asn 130 135 140	432
GGC ACA TTG GTG CCC GGG TTG AAA AGC CTC GTG TTG GGT GGC AGA AAA Gly Thr Leu Val Pro Gly Leu Lys Ser Leu Val Leu Gly Gly Arg Lys 145 150 155 160	480
GCT GTT AAA CAG GGA GTG GTA AAC CTT GTC AAA TAT GCC AAA Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys 165 170	522
TAA	525

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met Gly Ser Ser Leu Asp Asp Phe Cys His Asp Ser Thr Ala Pro Gln
1 5 10 15

Lys Val Leu Leu Ala Phe Ser Ile Thr Tyr Thr Pro Val Met Ile Tyr
20 25 30

Ala Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Leu Leu
35 40 45

Ile Phe Leu Asn Cys Ala Phe Thr Phe Gly Tyr Met Thr Phe Val His
50 55 60

Phe Gln Ser Thr Asn Lys Val Ala Leu Thr Met Gly Ala Val Val Ala
65 70 75 80

Leu Leu Trp Gly Val Tyr Ser Ala Ile Glu Thr Trp Lys Phe Ile Thr
85 90 95

Ser Arg Cys Arg Leu Cys Leu Leu Gly Arg Lys Tyr Ile Leu Ala Pro
100 105 110

Ala His His Val Glu Ser Ala Ala Gly Phe His Pro Ile Ala Ala Asn
115 120 125

Asp Asn His Ala Phe Val Val Arg Arg Pro Gly Ser Thr Thr Val Asn
130 135 140

Gly Thr Leu Val Pro Gly Leu Lys Ser Leu Val Leu Gly Gly Arg Lys
145 150 155 160

Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys
165 170

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-22 (VR 2429)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ATG	GGG	TCG	TCC	TTA	GAT	GAC	TTC	TGT	CAT	GAC	AGC	ACG	GCT	CCA	CAA	48
Met	Gly	Ser	Ser	Leu	Asp	Asp	Phe	Cys	His	Asp	Ser	Thr	Ala	Pro	Gln	
1				5					10					15		
AAG	GTG	CTT	TTG	GCG	TTT	TCT	ATT	ACC	TAC	ACG	CCA	GTG	ATG	ATA	TAT	96
Lys	Val	Leu	Leu	Ala	Phe	Ser	Ile	Thr	Tyr	Thr	Pro	Val	Met	Ile	Tyr	
				20				25				30				
GCC	CTG	AAG	GTG	AGT	CGC	GGC	CGA	CTG	CTA	GGG	CTT	CTG	CAC	CTT	TTG	144
Ala	Leu	Lys	Val	Ser	Arg	Gly	Arg	Leu	Leu	Gly	Leu	Leu	His	Leu	Leu	
		35				40						45				
ATC	TTC	CTG	AAT	TGT	GCT	TTC	ACC	TTC	GGG	TAC	ATG	ACA	TTC	GTG	CAC	192
Ile	Phe	Leu	Asn	Cys	Ala	Phe	Thr	Phe	Gly	Tyr	Met	Thr	Phe	Val	His	
		50			55					60						
TTT	CAG	AGT	ACA	AAT	AAG	GTC	GCA	CTC	ACT	ATG	GGA	GCA	GTA	GTT	GCA	240
Phe	Gln	Ser	Thr	Asn	Lys	Val	Ala	Leu	Thr	Met	Gly	Ala	Val	Val	Ala	
		65			70			75			80					
CTC	CTT	TGG	GGG	GTG	TAC	TCA	GCC	ATA	GAA	ACC	TGG	AAA	TTC	ATC	ACC	288
Leu	Leu	Trp	Gly	Val	Tyr	Ser	Ala	Ile	Glu	Thr	Trp	Lys	Phe	Ile	Thr	
		85			90							95				
TCC	AGA	TGC	CGT	TTG	TGC	TTG	CTA	GGC	CGC	AAG	TAC	ATT	CTG	GCC	CCT	336
Ser	Arg	Cys	Arg	Leu	Cys	Leu	Leu	Gly	Arg	Lys	Tyr	Ile	Leu	Ala	Pro	
		100				105						110				
GCC	CAC	CAC	GTT	GAA	AGT	GCC	GCA	GGC	TTT	CAT	CCG	ATT	GCG	GCA	AAT	384
Ala	His	His	Val	Glu	Ser	Ala	Ala	Gly	Phe	His	Pro	Ile	Ala	Ala	Asn	
		115			120							125				
GAT	AAC	CAC	GCA	TTT	GTC	GTT	CGG	CGT	CCC	GGC	TCC	ACT	ACG	GTC	AAC	432
Asp	Asn	His	Ala	Phe	Val	Val	Arg	Arg	Pro	Gly	Ser	Thr	Thr	Val	Asn	
		130			135						140					

GGC ACA TTG GTG CCC GGG TTG AAA AGC CTC GTG TTG GGT GGC AGA AAA	480
Gly Thr Leu Val Pro Gly Leu Lys Ser Leu Val Leu Gly Gly Arg Lys	
145 150 155 160	
GCT GTT AAA CAG GGA GTG GTA AAC CTT GTC AAA TAT GCC AAA	522
Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys	
165 170	
TAA	525

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 174 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met Gly Ser Ser Leu Asp Asp Phe Cys His Asp Ser Thr Ala Pro Gln	
1 5 10 15	
Lys Val Leu Leu Ala Phe Ser Ile Thr Tyr Thr Pro Val Met Ile Tyr	
20 25 30	
Ala Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Leu Leu	
35 40 45	
Ile Phe Leu Asn Cys Ala Phe Thr Phe Gly Tyr Met Thr Phe Val His	
50 55 60	
Phe Gln Ser Thr Asn Lys Val Ala Leu Thr Met Gly Ala Val Val Ala	
65 70 75 80	
Leu Leu Trp Gly Val Tyr Ser Ala Ile Glu Thr Trp Lys Phe Ile Thr	
85 90 95	
Ser Arg Cys Arg Leu Cys Leu Leu Gly Arg Lys Tyr Ile Leu Ala Pro	
100 105 110	
Ala His His Val Glu Ser Ala Ala Gly Phe His Pro Ile Ala Ala Asn	
115 120 125	
Asp Asn His Ala Phe Val Val Arg Arg Pro Gly Ser Thr Thr Val Asn	
130 135 140	
Gly Thr Leu Val Pro Gly Leu Lys Ser Leu Val Leu Gly Gly Arg Lys	
145 150 155 160	

Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys
165 170

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-79

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ATG GGG TCG TCC TTA GAT GAC TTC TGT TAT GAT AGT ACG GCT CCA CAA	48
Met Gly Ser Ser Leu Asp Asp Phe Cys Tyr Asp Ser Thr Ala Pro Gln	
1 5 10 15	
AAG GTG CTT TTG GCA TTT TCT ATT ACC TAC ACG CCA GTA ATG ATA TAT	96
Lys Val Leu Ala Phe Ser Ile Thr Tyr Thr Pro Val Met Ile Tyr	
20 25 30	
GCC CTA AAG GTG AGT CGC GGC CGA CTG CTA GGG CTT CTG CAC CTT TTG	144
Ala Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Leu Leu	
35 40 45	
ATT TTC CTG AAC TGT GCT TTC ACC TTC GGG TAC ATG ACA TTC ATG CAC	192
Ile Phe Leu Asn Cys Ala Phe Thr Phe Gly Tyr Met Thr Phe Met His	
50 55 60	
TTT CAG AGT ACA AAT AAG GTC GCG CTC ACT ATG GGA GCA GTA GTT GCA	240
Phe Gln Ser Thr Asn Lys Val Ala Leu Thr Met Gly Ala Val Val Ala	
65 70 75 80	
CTC CTT TGG GGG GTG TAC TCA GCC ATA GAA ACC TGG AAA TTC ATC ACC	288
Leu Leu Trp Gly Val Tyr Ser Ala Ile Glu Thr Trp Lys Phe Ile Thr	
85 90 95	

TCC AGA TGC CGT TTG TGC TTG CTA GGC CGC AAG TAC ATT CTG GCC CCT	336
Ser Arg Cys Arg Leu Cys Leu Leu Gly Arg Lys Tyr Ile Leu Ala Pro	
100 105 110	
GCC CAC CAC GTT GAA AGT GCC GCA GGC TTT CAT CCG ATT GCG GCA AAT	384
Ala His His Val Glu Ser Ala Ala Gly Phe His Pro Ile Ala Ala Asn	
115 120 125	
GAT AAC CAC GCA TTT GTC GTC CGG CGT CCC GGC TCC ACT ACG GTC AAC	432
Asp Asn His Ala Phe Val Val Arg Arg Pro Gly Ser Thr Thr Val Asn	
130 135 140	
GGC ACA TTG GTG CCC GGG TTG AAA AGC CTC GTG TTG GGT GGC AGA AAA	480
Gly Thr Leu Val Pro Gly Leu Lys Ser Leu Val Leu Gly Gly Arg Lys	
145 150 155 160	
GCT GTT AAA CAG GGA GTG GTA AAC CTT GTC AAA TAT GCC AAA	522
Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys	
165 170	
TAA	525

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 174 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met Gly Ser Ser Leu Asp Asp Phe Cys Tyr Asp Ser Thr Ala Pro Gln	
1 5 10 15	
Lys Val Leu Leu Ala Phe Ser Ile Thr Tyr Thr Pro Val Met Ile Tyr	
20 25 30	
Ala Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Leu Leu	
35 40 45	
Ile Phe Leu Asn Cys Ala Phe Thr Phe Gly Tyr Met Thr Phe Met His	
50 55 60	
Phe Gln Ser Thr Asn Lys Val Ala Leu Thr Met Gly Ala Val Val Ala	
65 70 75 80	
Leu Leu Trp Gly Val Tyr Ser Ala Ile Glu Thr Trp Lys Phe Ile Thr	
85 90 95	

Ser Arg Cys Arg Leu Cys Leu Leu Gly Arg Lys Tyr Ile Leu Ala Pro
100 105 110

Ala His His Val Glu Ser Ala Ala Gly Phe His Pro Ile Ala Ala Asn
115 120 125

Asp Asn His Ala Phe Val Val Arg Arg Pro Gly Ser Thr Thr Val Asn
130 135 140

Gly Thr Leu Val Pro Gly Leu Lys Ser Leu Val Leu Gly Gly Arg Lys
145 150 155 160

Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys
165 170

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-55 (VR 2430)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ATG GGG TCG TCC TTA GAT GAC TTC TGC CAT GAT AGC ACG GCT CCA CAA 48
Met Gly Ser Ser Leu Asp Asp Phe Cys His Asp Ser Thr Ala Pro Gln
1 5 10 15

AAG GTG CTT TTG GCG TTC TCT ATT ACC TAC ACG CCA GTG ATG ATA TAT 96
Lys Val Leu Leu Ala Phe Ser Ile Thr Tyr Thr Pro Val Met Ile Tyr
20 25 30

GCC CTA AAA GTA AGT CGC GGC CGA CTG CTA GGG CTT CTG CAC CTT TTG 144
Ala Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Leu Leu
35 40 45

ATC TTC CTA AAT TGT GCT TTC ACC TTC GGG TAC ATG ACA TTC GTG CAC Ile Phe Leu Asn Cys Ala Phe Thr Phe Gly Tyr Met Thr Phe Val His	192
50 55 60	
TTT CAG AGC ACA AAC AAG GTC GCG CTC ACT ATG GGA GCA GTA GTT GCA Phe Gln Ser Thr Asn Lys Val Ala Leu Thr Met Gly Ala Val Val Ala	240
65 70 75 80	
CTC CTT TGG GGG GTG TAC TCA GCC ATA GAA ACC TGG AAA TTC ATC ACC Leu Leu Trp Gly Val Tyr Ser Ala Ile Glu Thr Trp Lys Phe Ile Thr	288
85 90 95	
TCC AGA TGC CGT TTG TGC TTG CTA GGC CGC AAG TAC ATT TTG GCC CCT Ser Arg Cys Arg Leu Cys Leu Leu Gly Arg Lys Tyr Ile Leu Ala Pro	336
100 105 110	
GCC CAC CAC GTT GAA AGT GCC GCA GGC TTT CAT CCG ATA GCG GCA AAT Ala His His Val Glu Ser Ala Ala Gly Phe His Pro Ile Ala Ala Asn	384
115 120 125	
GAT AAC CAC GCA TTT GTC GTC CGG CGT CCC GGC TCC ACT ACG GTT AAC Asp Asn His Ala Phe Val Val Arg Arg Pro Gly Ser Thr Thr Val Asn	432
130 135 140	
GGC ACA TTG GTG CCC GGG TTG AAA AGC CTC GTG TTG GGT GGC AGA AAA Gly Thr Leu Val Pro Gly Leu Lys Ser Leu Val Leu Gly Gly Arg Lys	480
145 150 155 160	
GCT GTC AAA CAG GGA GTG GTA AAC CTT GTT AAA TAT GCC AAA Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys	522
165 170	
TAA	525

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 174 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met Gly Ser Ser Leu Asp Asp Phe Cys His Asp Ser Thr Ala Pro Gln	
1 5 10 15	
Lys Val Leu Leu Ala Phe Ser Ile Thr Tyr Thr Pro Val Met Ile Tyr	
20 25 30	

Ala Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Leu Leu
35 40 45

Ile Phe Leu Asn Cys Ala Phe Thr Phe Gly Tyr Met Thr Phe Val His
50 55 60

Phe Gln Ser Thr Asn Lys Val Ala Leu Thr Met Gly Ala Val Val Ala
65 70 75 80

Leu Leu Trp Gly Val Tyr Ser Ala Ile Glu Thr Trp Lys Phe Ile Thr
85 90 95

Ser Arg Cys Arg Leu Cys Leu Leu Gly Arg Lys Tyr Ile Leu Ala Pro
100 105 110

Ala His His Val Glu Ser Ala Ala Gly Phe His Pro Ile Ala Ala Asn
115 120 125

Asp Asn His Ala Phe Val Val Arg Arg Pro Gly Ser Thr Thr Val Asn
130 135 140

Gly Thr Leu Val Pro Gly Leu Lys Ser Leu Val Leu Gly Gly Arg Lys
145 150 155 160

Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys
165 170

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-3927 (VR 2431)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ATG GGG TCG TCC CTA GAC GAC TTT TGC AAT GAT AGC ACG GCT CCA CAA Met Gly Ser Ser Leu Asp Asp Phe Cys Asn Asp Ser Thr Ala Pro Gln	1	5	10	15	48
AAG GTG CTT TTG GCG TTT TCT ATT ACC TAC ACG CCG GTG ATG ATA TAT Lys Val Leu Leu Ala Phe Ser Ile Thr Tyr Thr Pro Val Met Ile Tyr	20	25	30		96
GCT CTA AAG GTA AGT CGC GGC CGA CTG CTA GGG CTT CTG CAC CTT TTG Ala Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Leu Leu	35	40	45		144
ATT TTT CTG AAT TGT GCT TTT ACT TTC GGG TAC ATG ACA TTC GTG CAC Ile Phe Leu Asn Cys Ala Phe Thr Phe Gly Tyr Met Thr Phe Val His	50	55	60		192
TTT GAG AGC ACA AAT AGG GTC GCG CTC ACT ATG GGA GCA GTA GTC GCA Phe Glu Ser Thr Asn Arg Val Ala Leu Thr Met Gly Ala Val Val Ala	65	70	75	80	240
CTT CTC TGG GGG GTG TAC TCA GCC ATA GAA ACC TGG AAA TTC ATC ACC Leu Leu Trp Gly Val Tyr Ser Ala Ile Glu Thr Trp Lys Phe Ile Thr	85	90	95		288
TCC AGA TGC CGT TTG TGC TTG CTA GGC CGC AAG TAC ATT CTG GCC CCT Ser Arg Cys Arg Leu Cys Leu Leu Gly Arg Lys Tyr Ile Leu Ala Pro	100	105	110		336
GCC CAC CAC GTT GAG AGT GCC GCA GGC TTT CAT CCG ATT GCG GCA AAT Ala His His Val Glu Ser Ala Ala Gly Phe His Pro Ile Ala Ala Asn	115	120	125		384
GAT AAC CAC GCA TTT GTC GTC CGG CGT CCC GGC TCC ACT ACG GTT AAC Asp Asn His Ala Phe Val Val Arg Arg Pro Gly Ser Thr Thr Val Asn	130	135	140		432
GGC ACA TTG GTG CCC GGG TTG AGA AGC CTC GTG TTG GGT GGC AAA AAA Gly Thr Leu Val Pro Gly Leu Arg Ser Leu Val Leu Gly Gly Lys Lys	145	150	155	160	480
GCT GTT AAG CAG GGA GTG GTA AAC CTT GTT AAA TAT GCC AAA Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys	165	170			522
TAA					525

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met Gly Ser Ser Leu Asp Asp Phe Cys Asn Asp Ser Thr Ala Pro Gln
1 5 10 15

Lys Val Leu Leu Ala Phe Ser Ile Thr Tyr Thr Pro Val Met Ile Tyr
20 25 30

Ala Leu Lys Val Ser Arg Gly Arg Leu Leu Gly Leu Leu His Leu Leu
35 40 45

Ile Phe Leu Asn Cys Ala Phe Thr Phe Gly Tyr Met Thr Phe Val His
50 55 60

Phe Glu Ser Thr Asn Arg Val Ala Leu Thr Met Gly Ala Val Val Ala
65 70 75 80

Leu Leu Trp Gly Val Tyr Ser Ala Ile Glu Thr Trp Lys Phe Ile Thr
85 90 95

Ser Arg Cys Arg Leu Cys Leu Leu Gly Arg Lys Tyr Ile Leu Ala Pro
100 105 110

Ala His His Val Glu Ser Ala Ala Gly Phe His Pro Ile Ala Ala Asn
115 120 125

Asp Asn His Ala Phe Val Val Arg Arg Pro Gly Ser Thr Thr Val Asn
130 135 140

Gly Thr Leu Val Pro Gly Leu Arg Ser Leu Val Leu Gly Gly Lys Lys
145 150 155 160

Ala Val Lys Gln Gly Val Val Asn Leu Val Lys Tyr Ala Lys
165 170

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-1894

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATG CCA AAT AAC AAC GGC AAG CAG CAG AAG AGA AAG AAG GGG GAT GGC Met Pro Asn Asn Asn Gly Lys Gln Gln Lys Arg Lys Lys Gly Asp Gly 1 5 10 15	48
CAG CCA GTC AAT CAG CTG TGC CAG ATG CTG GGT AAG ATC ATC GCT CAG Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala Gln 20 25 30	96
CAA AAC CAG TCC AGA GGC AAG GGA CCG GGA AAG AAA AAC AAG AAG AAA Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys Lys 35 40 45	144
AAC CCG GAG AAG CCC CAT TTT CCT CTA GCG ACT GAA GAT GAT GTC AGA Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg 50 55 60	192
CAT CAC TTC ACC CCT AGT GAG CGG CAA TTG TGT CTG TCG TCA ATC CAG His His Phe Thr Pro Ser Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln 65 70 75 80	240
ACC GCC TTT AAT CAA GGC GCT GGG ACT TGC ACC CTG TCA GAT TCA GGG Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Thr Leu Ser Asp Ser Gly 85 90 95	288
AGG ATA AGT TAC ACT GTG GAG TTT AGT TTG CCA ACG CAT CAT ACT GTG Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val 100 105 110	336
CGC TTG ATC CGC GTC ACA GCA TCA CCC TCA GCA TGA Arg Leu Ile Arg Val Thr Ala Ser Pro Ser Ala 115 120	372

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met Pro Asn Asn Asn Gly Lys Gln Gln Lys Arg Lys Lys Gly Asp Gly
1 5 10 15

Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala Gln
20 25 30

Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys Lys
35 40 45

Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg
50 55 60

His His Phe Thr Pro Ser Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln
65 70 75 80

Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Thr Leu Ser Asp Ser Gly
85 90 95

Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val
100 105 110

Arg Leu Ile Arg Val Thr Ala Ser Pro Ser Ala
115 120

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-22 (VR 2429)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATG CCA AAT AAC AAC GGT AAG CAG CAG AAG AGA AAG AAG GGG GAT GGC	48
Met Pro Asn Asn Asn Gly Lys Gln Gln Lys Arg Lys Lys Gly Asp Gly	
1 5 10 15	
CAG CCA GTC AAT CAG CTG TGC CAG ATG CTG GGC AAG ATC ATC GCT CAG	96
Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala Gln	
20 25 30	
CAA AAT CAG TCC AGA GGC AAG GGA CCG GGA AAG AAA AAT AAG AAG AAA	144
Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys Lys	
35 40 45	
AAC CCG GAG AAG CCC CAT TTT CCT CTA GCG ACT GAA GAT GAT GTC AGA	192
Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg	
50 55 60	
CAT CAC TTT ACC CCT AGT GAG CGG CAA TTG TGT CTG TCG TCA ATC CAG	240
His His Phe Thr Pro Ser Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln	
65 70 75 80	
ACC GCC TTT AAT CAA GGC GCT GGG ACT TGC ACC CTG TCA GAT TCA GGG	288
Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Thr Leu Ser Asp Ser Gly	
85 90 95	
AGG ATA AGT TAC ACT GTG GAG TTT AGT TTG CCT ACG CAT CAT ACT GTG	336
Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val	
100 105 110	
CGC CTG ATC CGC GTC ACA GCA TCA CCC TCA GCA TGA	372
Arg Leu Ile Arg Val Thr Ala Ser Pro Ser Ala	
115 120	

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Met Pro Asn Asn Asn Gly Lys Gln Gln Lys Arg Lys Lys Gly Asp Gly
1 5 10 15

Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala Gln
20 25 30

Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys Lys
35 40 45

Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg
50 55 60

His His Phe Thr Pro Ser Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln
65 70 75 80

Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Thr Leu Ser Asp Ser Gly
85 90 95

Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val
100 105 110

Arg Leu Ile Arg Val Thr Ala Ser Pro Ser Ala
115 120

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-79

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

ATG CCA AAT AAC AAC GGC AAG CAG CAG AAG AGA AAG AAG GGG GAT GGC	48
Met Pro Asn Asn Asn Gly Lys Gln Gln Lys Arg Lys Lys Gly Asp Gly	
1 5 10 15	
CAG CCA GTC AAT CAG CTG TGC CAG ATG CTG GGT AAG ATC ATC GCC CAG	96
Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala Gln	
20 25 30	
CAA AAC CAG TCT AGA GGC AAG GGA CCG GGA AAG AAA AAT AAG AAG AAA	144
Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys Lys	
35 40 45	
AAC CCG GAG AAG CCC CAT TTT CCT CTA GCG ACT GAA GAT GAT GTC AGA	192
Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg	
50 55 60	
CAT CAC TTT ACC CCT AGT GAG CGG CAA TTG TGT CTG TCG TCA ATC CAA	240
His His Phe Thr Pro Ser Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln	
65 70 75 80	
ACT GCC TTT AAT CAA GGC GCT GGG ACT TGC ACC CTG TCA GAT TCA GGG	288
Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Thr Leu Ser Asp Ser Gly	
85 90 95	
AGG ATA AGT TAC ACT GTG GAG TTT AGT TTG CCT ACG CAT CAT ACT GTG	336
Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val	
100 105 110	
CGC TTG ATC CGC GTC ACA GCA TCA CCC TCA GCA TGA	372
Arg Leu Ile Arg Val Thr Ala Ser Pro Ser Ala	
115 120	

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Met Pro Asn Asn Asn Gly Lys Gln Gln Lys Arg Lys Lys Gly Asp Gly	
1 5 10 15	
Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala Gln	
20 25 30	

Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys Lys
35 40 45

Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg
50 55 60

His His Phe Thr Pro Ser Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln
65 70 75 80

Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Thr Leu Ser Asp Ser Gly
85 90 95

Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val
100 105 110

Arg Leu Ile Arg Val Thr Ala Ser Pro Ser Ala
115 120

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-55 (VR 2430)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ATG CCA AAT AAC AAC GGC AAG CAG CAG AAG AAA AAG AAG GGG GAT GGC 48
Met Pro Asn Asn Asn Gly Lys Gln Gln Lys Lys Lys Lys Gly Asp Gly
1 5 10 15

CAG CCA GTC AAT CAG CTG TGC CAG ATG CTG GGT AAG ATC ATC GCT CAG 96
Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala Gln
20 25 30

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - ii) MOLECULE TYPE: protein
 - xii) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Met	Pro	Asn	Asn	Asn	Gly	Lys	Gln	Gln	Lys	Lys	Lys	Gly	Asp	Gly	
1					5				10				15		
Gln	Pro	Val	Asn	Gln	Leu	Cys	Gln	Met	Leu	Gly	Lys	Ile	Ile	Ala	Gln
					20				25				30		
Gln	Asn	Gln	Ser	Arg	Gly	Lys	Gly	Pro	Gly	Lys	Lys	Asn	Lys	Lys	Lys
					35				40				45		
Asn	Pro	Glu	Lys	Pro	His	Phe	Pro	Leu	Ala	Thr	Glu	Asp	Asp	Val	Arg
					50				55				60		
His	His	Phe	Thr	Ser	Gly	Glu	Arg	Gln	Leu	Cys	Leu	Ser	Ser	Ile	Gln
					65				70				75		

Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Thr Leu Ser Asp Ser Gly
85 90 95

Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val
100 105 110

Arg Leu Ile Arg Val Thr Ala Ser Pro Ser Ala
115 120

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-3927 (VR 2431)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATG CCA AAT AAC AAC GGC AAG CAG CAG AAG AAA AAG AAG GGG GAT GGC 48
Met Pro Asn Asn Asn Gly Lys Gln Gln Lys Lys Lys Lys Gly Asp Gly
1 5 10 15

CAG CCA GTC AAT CAG CTC TGC CAA ATG CTG GGT AAG ATC ATC GCC CAG 96
Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala Gln
20 25 30

CAA AAC CAG TCC AGA GGT AAG GGA CCG GGA AAG AAA AAT AAG AAG AAA 144
Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys Lys
35 40 45

AAC CCG GAG AAG CCC CAT TTT CCT CTA GCG ACT GAA GAT GAT GTC AGA 192
Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg
50 55 60

CAT CAC TTC ACC CCC AGT GAG CGG CAA TTG TGT CTG TCG TCA ATC CAG	240
His His Phe Thr Pro Ser Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln	
65 70 75 80	
ACT GCC TTT AAT CAG GGC GCT GGG ACC TGT ATC CTA TCA GAT TCA GGG	288
Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Ile Leu Ser Asp Ser Gly	
85 90 95	
AGG ATA AGT TAC ACT GTG GAG TTT AGT TTG CCG ACG CAT CAT ACT GTG	336
Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val	
100 105 110	
CGC CTG ATT CGC GTC ACG GCA CCA CCC TCA GCA TGA	372
Arg Leu Ile Arg Val Thr Ala Pro Pro Ser Ala	
115 120	

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Met Pro Asn Asn Asn Gly Lys Gln Gln Lys Lys Lys Lys Gly Asp Gly	
1 5 10 15	
Gln Pro Val Asn Gln Leu Cys Gln Met Leu Gly Lys Ile Ile Ala Gln	
20 25 30	
Gln Asn Gln Ser Arg Gly Lys Gly Pro Gly Lys Lys Asn Lys Lys Lys	
35 40 45	
Asn Pro Glu Lys Pro His Phe Pro Leu Ala Thr Glu Asp Asp Val Arg	
50 55 60	
His His Phe Thr Pro Ser Glu Arg Gln Leu Cys Leu Ser Ser Ile Gln	
65 70 75 80	
Thr Ala Phe Asn Gln Gly Ala Gly Thr Cys Ile Leu Ser Asp Ser Gly	
85 90 95	
Arg Ile Ser Tyr Thr Val Glu Phe Ser Leu Pro Thr His His Thr Val	
100 105 110	
Arg Leu Ile Arg Val Thr Ala Pro Pro Ser Ala	
115 120	

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Lys Lys Ser Thr Ala Pro Met
1 5

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ala Ser Gln Gly
1

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid;
(A) DESCRIPTION: DNA (synthetic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome
virus
(B) STRAIN: Iowa
(C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

TCTTCTTGCC TTTTCTATGC TTCTGAGATG AGTGAAAAGG GATTAAAGGT GGTATTTGGC	60
AATGTGTCAG GCATCGTGGC AGTGTGCGTC AACTTCACCA GTTACGTCCA ACATGTCAAG	120
GAATTTACCC AACGTTCCCTT GGTAGTTGAC CATGTGCGGC TGCTCCATT CATGACGCC	180
GAGACCATGA GGTGGGCAAC TGTTTAGCC TGTCTTTTA CCATTCTGTT GGCAATTGTA	240

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1799 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CCTGAATTGA GATGAAATGG GGTCTATGCA AAGCCTTTT GACAAAATTG GCCAACTTT	60
TGTGGATGCT TTCACGGAGT TCTTGGTGTC CATTGTTGAT ATCATTATAT TTTTGGCCAT	120
TTTGGTTGGC TTCACCATCG CAGGTTGGCT GGTGGTCTTT TGCATCAGAT TGGTTTGCTC	180
CGCGATACTC CGTGCAGGCC CTGCCATTCA CTCTGAGCAA TTACAGAAGA TCCTATGAGG	240
CCTTTCTCTC TCAGTGCCAG GTGGACATTC CCACCTGGGG AACTAACAT CCTTGAGGG	300
TGCTTGCGCA CCATAAGGTG TCAACCCCTGA TTGATGAAAT GGTGTCGCGT CGAATGTACC	360
GCATCATGGA AAAAGCAGGA CAGGCTGCCT GGAAACAGGT AGTGAGCGAG GCTACGCTGT	420
CTCGCATTAG TAGTTGGAT GTGGTGGCTC ATTTTCAGCA TCTTGCGGCC ATTGAAGCCG	480
AGACCTGTAA ATATCTGGCC TCTCGGCTGC CCATGCTACA CCACCTGCGC ATGACAGGGT	540
CAAATGTAAC CATAGTGTAT AATAGTACTT TGAATCAGGT GTTTGCTGTT TTCCCAACCC	600
CTGGTTCCCG GCCAAAGCTT CATGATTCC AGCAATGGCT AATAGCTGTA CATTCCCTCTA	660

TATTTTCCTC TGTTGCAGCT TCTTGTACTC TTTTTGTTGT GCTGTGGTTG CGGGTTCCAA	720
TGCTACGTAC TGTTTTGGT TTCCGCTGGT TAGGGGCAAT TTTTCTTCG AACTCACCGT	780
GAATTACACG GTGTGCCCGC CTTGCCTCAC CCGGCAAGCA GCCGCAGAGG CCTACGAACC	840
CGGCAGGTCC CTTGGTGCA GGATAGGGCA TGATCGATGT GGGGAGGACG ATCATGATGA	900
ACTAGGGTTT GTGGTGCCGT CTGGCCTCTC CAGCGAAGGC CACTTGACCA GTGCTTACGC	960
CTGGTTGGCG TCCCTGTCT TCAGCTATAAC GGCCCAGTTC CATCCCGAGA TATTCGGGAT	1020
AGGGAATGTG AGTCGAGTCT ATGTTGACAT CAAGCACCAA TTCATTGCG CTGTTCATGA	1080
TGGGCAGAAC ACCACCTTGC CCCACCATGA CAACATTCA GCCGTGCTTC AGACCTATTA	1140
CCAGCATCAG GTCGACGGGG GCAATTGGTT TCACCTAGAA TGGGTGCGTC CCTTCTTTTC	1200
CTCTTGGTTG GTTTAAATG TCTCTTGGTT TCTCAGGCCT TCGCCTGCAA GCCATGTTTC	1260
AGTCGAGTC TTTCAGACAT CAAGACCAAC ACCACCGCAG CGGCAGGCTT TGCTGTCCTC	1320
CAAGACATCA GTTGCCTTAG GCATCGAAC TCGGCCTCTG AGGCGATTG CAAAGTCCTC	1380
CAGTGCCGCA CGGCGATAGG GACACCCGTG TATATCACTG TCACAGCCAA TGTTACCGAT	1440
GAGAATTATT TGCATTCCTC TGATCTTCTC ATGCTTCTT CTTGCCTTTT CTATGCTTCT	1500
GAGATGAGTG AAAAGGGATT TAAGGTGGTA TTTGGCAATG TGTCAGGCAT CGTGGCAGTG	1560
TGCGTCAACT TCACCAGTTA CGTCCAACAT GTCAAGGAAT TTACCCAACG TTCCTTGGTA	1620
GTTGACCATG TGCGGCTGCT CCATTCATG ACGCCCGAGA CCATGAGGTG GGCAACTGTT	1680
TTAGCCTGTC TTTTACCAT TCTGTTGGCA ATTTGAATGT TTAAGTATGT TGGGGAAATG	1740
CTTGACCGCG GGCTGTTGCT CGCAATTGCT TTTTTATGG TGTATCGTGC CGTCTTGT	1799

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa

(C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ATG AAA TGG GGT CTA TGC AAA GCC TTT TTG ACA AAA TTG GCC AAC TTT Met Lys Trp Gly Leu Cys Lys Ala Phe Leu Thr Lys Leu Ala Asn Phe 1 5 10 15	48
TTG TGG ATG CTT TCA CGG AGT TCT TGG TGT CCA TTG TTG ATA TCA TTA Leu Trp Met Leu Ser Arg Ser Ser Trp Cys Pro Leu Leu Ile Ser Leu 20 25 30	96
TAT TTT TGG CCA TTT TGT TTG GCT TCA CCA TCG CAG GTT GGC TGG TGG Tyr Phe Trp Pro Phe Cys Leu Ala Ser Pro Ser Gln Val Gly Trp Trp 35 40 45	144
TCT TTT GCA TCA GAT TGG TTT GCT CCG CGA TAC TCC GTG CGC GCC CTG Ser Phe Ala Ser Asp Trp Phe Ala Pro Arg Tyr Ser Val Arg Ala Leu 50 55 60	192
CCA TTC ACT CTG AGC AAT TAC AGA AGA TCC TAT GAG GCC TTT CTC TCT Pro Phe Thr Leu Ser Asn Tyr Arg Arg Ser Tyr Glu Ala Phe Leu Ser 65 70 75 80	240
CAG TGC CAG GTG GAC ATT CCC ACC TGG GGA ACT AAA CAT CCT TTG GGG Gln Cys Gln Val Asp Ile Pro Thr Trp Gly Thr Lys His Pro Leu Gly 85 90 95	288
ATG CTT TGG CAC CAT AAG GTG TCA ACC CTG ATT GAT GAA ATG GTG TCG Met Leu Trp His His Lys Val Ser Thr Leu Ile Asp Glu Met Val Ser 100 105 110	336
CGT CGA ATG TAC CGC ATC ATG GAA AAA GCA GGA CAG GCT GCC TGG AAA Arg Arg Met Tyr Arg Ile Met Glu Lys Ala Gly Gln Ala Ala Trp Lys 115 120 125	384
CAG GTA GTG AGC GAG GCT ACG CTG TCT CGC ATT AGT AGT TTG GAT GTG Gln Val Val Ser Glu Ala Thr Leu Ser Arg Ile Ser Ser Leu Asp Val 130 135 140	432
GTG GCT CAT TTT CAG CAT CTT GCC GCC ATT GAA GCC GAG ACC TGT AAA Val Ala His Phe Gln His Leu Ala Ala Ile Glu Ala Glu Thr Cys Lys 145 150 155 160	480

TAT CTG GCC TCT CCG CTG CCC ATG CTA CAC CAC CTG CGC ATG ACA GGG Tyr Leu Ala Ser Arg Leu Pro Met Leu His His Leu Arg Met Thr Gly	528
165 170 175	
TCA AAT GTA ACC ATA GTG TAT AAT AGT ACT TTG AAT CAG GTG TTT GCT Ser Asn Val Thr Ile Val Tyr Asn Ser Thr Leu Asn Gln Val Phe Ala	576
180 185 190	
GTT TTC CCA ACC CCT GGT TCC CGG CCA AAG CTT CAT GAT TTC CAG CAA Val Phe Pro Thr Pro Gly Ser Arg Pro Lys Leu His Asp Phe Gln Gln	624
195 200 205	
TGG CTA ATA GCT GTA CAT TCC TCT ATA TTT TCC TCT GTT GCA GCT TCT Trp Leu Ile Ala Val His Ser Ser Ile Phe Ser Ser Val Ala Ala Ser	672
210 215 220	
TGT ACT CTT TTT GTT GTG CTG TGG TTG CGG GTT CCA ATG CTA CGT ACT Cys Thr Leu Phe Val Val Leu Trp Leu Arg Val Pro Met Leu Arg Thr	720
225 230 235 240	
GTT TTT GGT TTC CGC TGG TTA GGG GCA ATT TTT CTT TCG AAC TCA CGG Val Phe Gly Phe Arg Trp Leu Gly Ala Ile Phe Leu Ser Asn Ser Arg	768
245 250 255	
TGA	771

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 256 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met Lys Trp Gly Leu Cys Lys Ala Phe Leu Thr Lys Leu Ala Asn Phe	
1 5 10 15	
Leu Trp Met Leu Ser Arg Ser Ser Trp Cys Pro Leu Leu Ile Ser Leu	
20 25 30	
Tyr Phe Trp Pro Phe Cys Leu Ala Ser Pro Ser Gln Val Gly Trp Trp	
35 40 45	
Ser Phe Ala Ser Asp Trp Phe Ala Pro Arg Tyr Ser Val Arg Ala Leu	
50 55 60	
Pro Phe Thr Leu Ser Asn Tyr Arg Arg Ser Tyr Glu Ala Phe Leu Ser	
65 70 75 80	

Gln Cys Gln Val Asp Ile Pro Thr Trp Gly Thr Lys His Pro Leu Gly
85 90 95

Met Leu Trp His His Lys Val Ser Thr Leu Ile Asp Glu Met Val Ser
100 105 110

Arg Arg Met Tyr Arg Ile Met Glu Lys Ala Gly Gln Ala Ala Trp Lys
115 120 125

Gln Val Val Ser Glu Ala Thr Leu Ser Arg Ile Ser Ser Leu Asp Val
130 135 140

Val Ala His Phe Gln His Leu Ala Ala Ile Glu Ala Glu Thr Cys Lys
145 150 155 160

Tyr Leu Ala Ser Arg Leu Pro Met Leu His His Leu Arg Met Thr Gly
165 170 175

Ser Asn Val Thr Ile Val Tyr Asn Ser Thr Leu Asn Gln Val Phe Ala
180 185 190

Val Phe Pro Thr Pro Gly Ser Arg Pro Lys Leu His Asp Phe Gln Gln
195 200 205

Trp Leu Ile Ala Val His Ser Ser Ile Phe Ser Ser Val Ala Ala Ser
210 215 220

Cys Thr Leu Phe Val Val Leu Trp Leu Arg Val Pro Met Leu Arg Thr
225 230 235 240

Val Phe Gly Phe Arg Trp Leu Gly Ala Ile Phe Leu Ser Asn Ser Arg
245 250 255

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 765 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: porcine reproductive and respiratory syndrome virus
 - (B) STRAIN: Iowa
 - (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS

(B) LOCATION: 1..762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ATG GCT AAT AGC TGT ACA TTC CTC TAT ATT TTC CTC TGT TGC AGC TTC Met Ala Asn Ser Cys Thr Phe Leu Tyr Ile Phe Leu Cys Cys Ser Phe 1 5 10 15	48
TTG TAC TCT TTT TGT TGT GCT GTG GTT GCG GGT TCC AAT GCT ACG TAC Leu Tyr Ser Phe Cys Cys Ala Val Val Ala Gly Ser Asn Ala Thr Tyr 20 25 30	96
TGT TTT TGG TTT CCG CTG GTT AGG GGC AAT TTT TCT TTC GAA CTC ACG Cys Phe Trp Phe Pro Leu Val Arg Gly Asn Phe Ser Phe Glu Leu Thr 35 40 45	144
GTG AAT TAC ACG GTG TGC CCG CCT TGC CTC ACC CGG CAA GCA GCC GCA Val Asn Tyr Thr Val Cys Pro Pro Cys Leu Thr Arg Gln Ala Ala Ala 50 55 60	192
GAG GCC TAC GAA CCC GGC AGG TCC CTT TGG TGC AGG ATA GGG CAT GAT Glu Ala Tyr Glu Pro Gly Arg Ser Leu Trp Cys Arg Ile Gly His Asp 65 70 75 80	240
CGA TGT GGG GAG GAC GAT CAT GAT GAA CTA GGG TTT GTG GTG CCG TCT Arg Cys Gly Glu Asp Asp His Asp Glu Leu Gly Phe Val Val Pro Ser 85 90 95	288
GGC CTC TCC AGC GAA GGC CAC TTG ACC AGT GCT TAC GCC TGG TTG GCG Gly Leu Ser Ser Glu Gly His Leu Thr Ser Ala Tyr Ala Trp Leu Ala 100 105 110	336
TCC CTG TCC TTC AGC TAT ACG GCC CAG TTC CAT CCC GAG ATA TTC GGG Ser Leu Ser Phe Ser Tyr Thr Ala Gln Phe His Pro Glu Ile Phe Gly 115 120 125	384
ATA GGG AAT GTG AGT CGA GTC TAT GTT GAC ATC AAG CAC CAA TTC ATT Ile Gly Asn Val Ser Arg Val Tyr Val Asp Ile Lys His Gln Phe Ile 130 135 140	432
TGC GCT GTT CAT GAT GGG CAG AAC ACC ACC TTG CCC CAC CAT GAC AAC Cys Ala Val His Asp Gly Gln Asn Thr Thr Leu Pro His His Asp Asn 145 150 155 160	480
ATT TCA GCC GTG CTT CAG ACC TAT TAC CAG CAT CAG GTC GAC GGG GGC Ile Ser Ala Val Leu Gln Thr Tyr Tyr Gln His Gln Val Asp Gly Gly 165 170 175	528
AAT TGG TTT CAC CTA GAA TGG GTG CGT CCC TTC TTT TCC TCT TGG TTG Asn Trp Phe His Leu Glu Trp Val Arg Pro Phe Phe Ser Ser Trp Leu 180 185 190	576

GTT TTA AAT GTC TCT TGG TTT CTC AGG CGT TCG CCT GCA AGC CAT GTT	624
Val Leu Asn Val Ser Trp Phe Leu Arg Arg Ser Pro Ala Ser His Val	
195 200 205	
TCA GTT CGA GTC TTT CAG ACA TCA AGA CCA ACA CCA CCG CAG CGG CAG	672
Ser Val Arg Val Phe Gln Thr Ser Arg Pro Thr Pro Pro Gln Arg Gln	
210 215 220	
GCT TTG CTG TCC TCC AAG ACA TCA GTT GCC TTA GGC ATC GCA ACT CGG	720
Ala Leu Leu Ser Ser Lys Thr Ser Val Ala Leu Gly Ile Ala Thr Arg	
225 230 235 240	
CCT CTG AGG CGA TTC GCA AAG TCC CTC AGT GCC GCA CGG CGA	762
Pro Leu Arg Arg Phe Ala Lys Ser Leu Ser Ala Ala Arg Arg	
245 250	
TAG	765

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 254 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met Ala Asn Ser Cys Thr Phe Leu Tyr Ile Phe Leu Cys Cys Ser Phe	
1 5 10 15	
Leu Tyr Ser Phe Cys Cys Ala Val Val Ala Gly Ser Asn Ala Thr Tyr	
20 25 30	
Cys Phe Trp Phe Pro Leu Val Arg Gly Asn Phe Ser Phe Glu Leu Thr	
35 40 45	
Val Asn Tyr Thr Val Cys Pro Pro Cys Leu Thr Arg Gln Ala Ala Ala	
50 55 60	
Glu Ala Tyr Glu Pro Gly Arg Ser Leu Trp Cys Arg Ile Gly His Asp	
65 70 75 80	
Arg Cys Gly Glu Asp Asp His Asp Glu Leu Gly Phe Val Val Pro Ser	
85 90 95	
Gly Leu Ser Ser Glu Gly His Leu Thr Ser Ala Tyr Ala Trp Leu Ala	
100 105 110	

Ser Leu Ser Phe Ser Tyr Thr Ala Gln Phe His Pro Glu Ile Phe Gly
115 120 125

Ile Gly Asn Val Ser Arg Val Tyr Val Asp Ile Lys His Gln Phe Ile
130 135 140

Cys Ala Val His Asp Gly Gln Asn Thr Thr Leu Pro His His Asp Asn
145 150 155 160

Ile Ser Ala Val Leu Gln Thr Tyr Tyr Gln His Gln Val Asp Gly Gly
165 170 175

Asn Trp Phe His Leu Glu Trp Val Arg Pro Phe Phe Ser Ser Trp Leu
180 185 190

Val Leu Asn Val Ser Trp Phe Leu Arg Arg Ser Pro Ala Ser His Val
195 200 205

Ser Val Arg Val Phe Gln Thr Ser Arg Pro Thr Pro Pro Gln Arg Gln
210 215 220

Ala Leu Leu Ser Ser Lys Thr Ser Val Ala Leu Gly Ile Ala Thr Arg
225 230 235 240

Pro Leu Arg Arg Phe Ala Lys Ser Leu Ser Ala Ala Arg Arg
245 250

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (B) STRAIN: Iowa
- (C) INDIVIDUAL ISOLATE: ISU-12 (VR 2385/VR 2386)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATG GGT GCG TCC CTT CTC TTG GTT GGT TTT AAA TGT CTC TTG Met Gly Ala Ser Leu Leu Phe Leu Leu Val Gly Phe Lys Cys Leu Leu	48
1 5 10 15	
GTT TCT CAG GCG TTC GCC TGC AAG CCA TGT TTC AGT TCG AGT CTT TCA Val Ser Gln Ala Phe Ala Cys Lys Pro Cys Phe Ser Ser Ser Leu Ser	96
20 25 30	
GAC ATC AAG ACC AAC ACC GCA GCG GCA GGC TTT GCT GTC CTC CAA Asp Ile Lys Thr Asn Thr Ala Ala Ala Gly Phe Ala Val Leu Gln	144
35 40 45	
GAC ATC AGT TGC CTT AGG CAT CGC AAC TCG GCC TCT GAG GCG ATT CGC Asp Ile Ser Cys Leu Arg His Arg Asn Ser Ala Ser Glu Ala Ile Arg	192
50 55 60	
AAA GTC CCT CAG TGC CGC ACG GCG ATA GGG ACA CCC GTG TAT ATC ACT Lys Val Pro Gln Cys Arg Thr Ala Ile Gly Thr Pro Val Tyr Ile Thr	240
65 70 75 80	
GTC ACA GCC AAT GTT ACC GAT GAG AAT TAT TTG CAT TCC TCT GAT CTT Val Thr Ala Asn Val Thr Asp Glu Asn Tyr Leu His Ser Ser Asp Leu	288
85 90 95	
CTC ATG CTT TCT TGC CTT TTC TAT GCT TCT GAG ATG AGT GAA AAG Leu Met Leu Ser Ser Cys Leu Phe Tyr Ala Ser Glu Met Ser Glu Lys	336
100 105 110	
GGA TTT AAG GTG GTA TTT GGC AAT GTG TCA GGC ATC GTG GCA GTG TGC Gly Phe Lys Val Val Phe Gly Asn Val Ser Gly Ile Val Ala Val Cys	384
115 120 125	
GTC AAC TTC ACC AGT TAC GTC CAA CAT GTC AAG GAA TTT ACC CAA CGT Val Asn Phe Thr Ser Tyr Val Gln His Val Lys Glu Phe Thr Gln Arg	432
130 135 140	
TCC TTG GTA GTT GAC CAT GTG CGG CTG CTC CAT TTC ATG ACG CCC GAG Ser Leu Val Val Asp His Val Arg Leu Leu His Phe Met Thr Pro Glu	480
145 150 155 160	
ACC ATG AGG TGG GCA ACT GTT TTA GCC TGT CTT TTT ACC ATT CTG TTG Thr Met Arg Trp Ala Thr Val Leu Ala Cys Leu Phe Thr Ile Leu Leu	528
165 170 175	
GCA ATT TGA Ala Ile	537

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Met Gly Ala Ser Leu Leu Phe Leu Leu Val Gly Phe Lys Cys Leu Leu
1 5 10 15

Val Ser Gln Ala Phe Ala Cys Lys Pro Cys Phe Ser Ser Ser Leu Ser
20 25 30

Asp Ile Lys Thr Asn Thr Thr Ala Ala Ala Gly Phe Ala Val Leu Gln
35 40 45

Asp Ile Ser Cys Leu Arg His Arg Asn Ser Ala Ser Glu Ala Ile Arg
50 55 60

Lys Val Pro Gln Cys Arg Thr Ala Ile Gly Thr Pro Val Tyr Ile Thr
65 70 75 80

Val Thr Ala Asn Val Thr Asp Glu Asn Tyr Leu His Ser Ser Asp Leu
85 90 95

Leu Met Leu Ser Ser Cys Leu Phe Tyr Ala Ser Glu Met Ser Glu Lys
100 105 110

Gly Phe Lys Val Val Phe Gly Asn Val Ser Gly Ile Val Ala Val Cys
115 120 125

Val Asn Phe Thr Ser Tyr Val Gln His Val Lys Glu Phe Thr Gln Arg
130 135 140

Ser Leu Val Val Asp His Val Arg Leu Leu His Phe Met Thr Pro Glu
145 150 155 160

Thr Met Arg Trp Ala Thr Val Leu Ala Cys Leu Phe Thr Ile Leu Leu
165 170 175

Ala Ile

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: porcine reproductive and respiratory syndrome virus
(C) INDIVIDUAL ISOLATE: Lelystad

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

ATG CAA TGG GGT CAC TGT GGA GTA AAA TCA GCC AGC TGT TCG TGG ACG	48
Met Gln Trp Gly His Cys Gly Val Lys Ser Ala Ser Cys Ser Trp Thr	
1 5 10 15	
CCT TCA CTG AGT TCC TTG TTA GTG TGG TTG ATA TTG CCA TTT TCC TTG	96
Pro Ser Leu Ser Ser Leu Leu Val Trp Leu Ile Leu Pro Phe Ser Leu	
20 25 30	
CCA TAC TGT TTG GGT TCA CCG TCG CAG GAT GGT TAC TGG TCT TTC TTC	144
Pro Tyr Cys Leu Gly Ser Pro Ser Gln Asp Gly Tyr Trp Ser Phe Phe	
35 40 45	
TCA GAG TGG TTT GCT CCG CGC TTC TCC GTT CGC GCT CTG CCA TTC ACT	192
Ser Glu Trp Phe Ala Pro Arg Phe Ser Val Arg Ala Leu Pro Phe Thr	
50 55 60	
CTC CCG AAC TAT CGA AGG TCC TAT GAA GGC TTG TTG CCC AAC TGC AGA	240
Leu Pro Asn Tyr Arg Arg Ser Tyr Glu Gly Leu Leu Pro Asn Cys Arg	
65 70 75 80	
CCG GAT GTC CCA CAA TTT GCA GTC AAG CAC CCA TTG GGT ATG TTT TGG	288
Pro Asp Val Pro Gln Phe Ala Val Lys His Pro Leu Gly Met Phe Trp	
85 90 95	
CAC ATG CGA GTT TCC CAC TTG ATT GAT GAG ATG GTC TCT CGT CGC ATT	336
His Met Arg Val Ser His Leu Ile Asp Glu Met Val Ser Arg Arg Ile	
100 105 110	
TAC CAG ACC ATG GAA CAT TCA GGT CAA GCG GCC TGG AAG CAG GTG GTT	384
Tyr Gln Thr Met Glu His Ser Gly Gln Ala Ala Trp Lys Gln Val Val	
115 120 125	
GGT GAG GCC ACT CTC ACG AAG CTG TCA GGG CTC GAT ATA GTT ACT CAT	432
Gly Glu Ala Thr Leu Thr Lys Leu Ser Gly Leu Asp Ile Val Thr His	
130 135 140	

TTC CAA CAC CTG GCC GCA GTG GAG GCG GAT TCT TGC CGC TTT CTC AGC Phe Gln His Leu Ala Ala Val Glu Ala Asp Ser Cys Arg Phe Leu Ser	145	150	155	160	480
TCA CGA CTC GTG ATG CTA AAA AAT CTT GCC GTT GGC AAT GTG AGC CTA Ser Arg Leu Val Met Leu Lys Asn Leu Ala Val Gly Asn Val Ser Leu	165	170	175		528
CAG TAC AAC ACC ACG TTG GAC CGC GTT GAG CTC ATC TTC CCC ACG CCA Gln Tyr Asn Thr Thr Leu Asp Arg Val Glu Leu Ile Phe Pro Thr Pro	180	185	190		576
GGT ACG AGG CCC AAG TTG ACC GAT TTC AGA CAA TGG CTC ATC AGT GTG Gly Thr Arg Pro Lys Leu Thr Asp Phe Arg Gln Trp Leu Ile Ser Val	195	200	205		624
CAC GCT TCC ATT TTT TCC TCT GTG GCT TCA TCT GTT ACC TTG TTC ATA His Ala Ser Ile Phe Ser Ser Val Ala Ser Ser Val Thr Leu Phe Ile	210	215	220		672
G TG CTT TGG CTT CGA ATT CCA GCT CTA CGC TAT GTT TTT GGT TTC CAT Val Leu Trp Leu Arg Ile Pro Ala Leu Arg Tyr Val Phe Gly Phe His	225	230	235	240	720
TGG CCC ACG GCA ACA CAT CAT TCG AGC TGA Trp Pro Thr Ala Thr His His Ser Ser	245				750

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 249 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Met Gln Trp Gly His Cys Gly Val Lys Ser Ala Ser Cys Ser Trp Thr	1	5	10	15
Pro Ser Leu Ser Ser Leu Leu Val Trp Leu Ile Leu Pro Phe Ser Leu	20	25	30	
Pro Tyr Cys Leu Gly Ser Pro Ser Gln Asp Gly Tyr Trp Ser Phe Phe	35	40	45	
Ser Glu Trp Phe Ala Pro Arg Phe Ser Val Arg Ala Leu Pro Phe Thr	50	55	60	

Leu Pro Asn Tyr Arg Arg Ser Tyr Glu Gly Leu Leu Pro Asn Cys Arg
65 70 75 80

Pro Asp Val Pro Gln Phe Ala Val Lys His Pro Leu Gly Met Phe Trp
85 90 95

His Met Arg Val Ser His Leu Ile Asp Glu Met Val Ser Arg Arg Ile
100 105 110

Tyr Gln Thr Met Glu His Ser Gly Gln Ala Ala Trp Lys Gln Val Val
115 120 125

Gly Glu Ala Thr Leu Thr Lys Leu Ser Gly Leu Asp Ile Val Thr His
130 135 140

Phe Gln His Leu Ala Ala Val Glu Ala Asp Ser Cys Arg Phe Leu Ser
145 150 155 160

Ser Arg Leu Val Met Leu Lys Asn Leu Ala Val Gly Asn Val Ser Leu
165 170 175

Gln Tyr Asn Thr Thr Leu Asp Arg Val Glu Leu Ile Phe Pro Thr Pro
180 185 190

Gly Thr Arg Pro Lys Leu Thr Asp Phe Arg Gln Trp Leu Ile Ser Val
195 200 205

His Ala Ser Ile Phe Ser Ser Val Ala Ser Ser Val Thr Leu Phe Ile
210 215 220

Val Leu Trp Leu Arg Ile Pro Ala Leu Arg Tyr Val Phe Gly Phe His
225 230 235 240

Trp Pro Thr Ala Thr His His Ser Ser
245

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: porcine reproductive and respiratory syndrome virus
- (C) INDIVIDUAL ISOLATE: Lelystad

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

ATG GCT CAT CAG TGT GCA CGC TTC CAT TTT TTC CTC TGT GGC TTC ATC Met Ala His Gln Cys Ala Arg Phe His Phe Phe Leu Cys Gly Phe Ile 1 5 10 15	48
TGT TAC CTT GTT CAT AGT GCT TTG GCT TCG AAT TCC AGC TCT ACG CTA Cys Tyr Leu Val His Ser Ala Leu Ala Ser Asn Ser Ser Thr Leu 20 25 30	96
TGT TTT TGG TTT CCA TTG GCC CAC GGC AAC ACA TCA TTC GAG CTG ACC Cys Phe Trp Phe Pro Leu Ala His Gly Asn Thr Ser Phe Glu Leu Thr 35 40 45	144
ATC AAC TAC ACC ATA TGC ATG CCC TGT TCT ACC AGT CAA GCG GCT CGC Ile Asn Tyr Thr Ile Cys Met Pro Cys Ser Thr Ser Gln Ala Ala Arg 50 55 60	192
CAA AGG CTC GAG CCC GGT CGT AAC ATG TGG TGC AAA ATA GGG CAT GAC Gln Arg Leu Glu Pro Gly Arg Asn Met Trp Cys Lys Ile Gly His Asp 65 70 75 80	240
AGG TGT GAG GAG CGT GAC CAT GAT GAG TTG TTA ATG TCC ATC CCG TCC Arg Cys Glu Glu Arg Asp His Asp Glu Leu Leu Met Ser Ile Pro Ser 85 90 95	288
GGG TAC GAC AAC CTC AAA CTT GAG GGT TAT TAT GCT TGG CTG GCT TTT Gly Tyr Asp Asn Leu Lys Leu Glu Gly Tyr Tyr Ala Trp Leu Ala Phe 100 105 110	336
TTG TCC TTT TCC TAC GCG GCC CAA TTC CAT CCG GAG TTG TTC GGG ATA Leu Ser Phe Ser Tyr Ala Ala Gln Phe His Pro Glu Leu Phe Gly Ile 115 120 125	384
GGG AAT GTG TCG CGC GTC TTC GTG GAC AAG CGA CAC CAG TTC ATT TGT Gly Asn Val Ser Arg Val Phe Val Asp Lys Arg His Gln Phe Ile Cys 130 135 140	432
GCC GAG CAT GAT GGA CAC AAT TCA ACC GTA TCT ACC GGA CAC AAC ATC Ala Glu His Asp Gly His Asn Ser Thr Val Ser Thr Gly His Asn Ile 145 150 155 160	480
TCC GCA TTA TAT GCG GCA TAT TAC CAC CAC CAA ATA GAC GGG GGC AAT Ser Ala Leu Tyr Ala Ala Tyr Tyr His His Gln Ile Asp Gly Gly Asn 165 170 175	528

TGG	TTC	CAT	TTG	GAA	TGG	CTG	CGG	CCA	CTC	TTT	TCT	TCC	TGG	CTG	GTG	576
Trp	Phe	His	Leu	Glu	Trp	Leu	Arg	Pro	Leu	Phe	Ser	Ser	Trp	Leu	Val	
			180					185					190			
CTC	AAC	ATA	TCA	TGG	TTT	CTG	AGG	CGT	TCG	CCT	GTA	AGC	CCT	GTT	TCT	624
Leu	Asn	Ile	Ser	Trp	Phe	Leu	Arg	Arg	Ser	Pro	Val	Ser	Pro	Val	Ser	
		195				200			205							
CGA	CGC	ATC	TAT	CAG	ATA	TTG	AGA	CCA	ACA	CGA	CCG	CGG	CTG	CCG	GTT	672
Arg	Arg	Ile	Tyr	Gln	Ile	Leu	Arg	Pro	Thr	Arg	Pro	Arg	Leu	Pro	Val	
		210				215			220							
TCA	TGG	TCC	TTC	AGG	ACA	TCA	ATT	GTT	TCC	GAC	CTC	ACG	GGG	TCT	CAG	720
Ser	Trp	Ser	Phe	Arg	Thr	Ser	Ile	Val	Ser	Asp	Leu	Thr	Gly	Ser	Gln	
		225		230			235			240						
CAG	CGC	AAG	AGA	AAA	TTT	CCT	TCG	GAA	AGT	CGT	CCC	AAT	GTC	GTG	AAG	768
Gln	Arg	Lys	Arg	Lys	Phe	Pro	Ser	Glu	Ser	Arg	Pro	Asn	Val	Val	Lys	
		245			250			255								
CCG	TCG	GTA	CTC	CCC	AGT	ACA	TCA	CGA	TAA							798
Pro	Ser	Val	Leu	Pro	Ser	Thr	Ser	Arg								
		260			265											

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Met	Ala	His	Gln	Cys	Ala	Arg	Phe	His	Phe	Phe	Leu	Cys	Gly	Phe	Ile	
1			5					10				15				
Cys	Tyr	Leu	Val	His	Ser	Ala	Leu	Ala	Ser	Asn	Ser	Ser	Ser	Thr	Leu	
			20				25					30				
Cys	Phe	Trp	Phe	Pro	Leu	Ala	His	Gly	Asn	Thr	Ser	Phe	Glu	Leu	Thr	
			35				40					45				
Ile	Asn	Tyr	Thr	Ile	Cys	Met	Pro	Cys	Ser	Thr	Ser	Gln	Ala	Ala	Arg	
			50			55					60					
Gln	Arg	Leu	Glu	Pro	Gly	Arg	Asn	Met	Trp	Cys	Lys	Ile	Gly	His	Asp	
			65		70			75				80				

Arg Cys Glu Glu Arg Asp His Asp Glu Leu Leu Met Ser Ile Pro Ser
85 90 95

Gly Tyr Asp Asn Leu Lys Leu Glu Gly Tyr Tyr Ala Trp Leu Ala Phe
100 105 110

Leu Ser Phe Ser Tyr Ala Ala Gln Phe His Pro Glu Leu Phe Gly Ile
115 120 125

Gly Asn Val Ser Arg Val Phe Val Asp Lys Arg His Gln Phe Ile Cys
130 135 140

Ala Glu His Asp Gly His Asn Ser Thr Val Ser Thr Gly His Asn Ile
145 150 155 160

Ser Ala Leu Tyr Ala Ala Tyr Tyr His His Gln Ile Asp Gly Gly Asn
165 170 175

Trp Phe His Leu Glu Trp Leu Arg Pro Leu Phe Ser Ser Trp Leu Val
180 185 190

Leu Asn Ile Ser Trp Phe Leu Arg Arg Ser Pro Val Ser Pro Val Ser
195 200 205

Arg Arg Ile Tyr Gln Ile Leu Arg Pro Thr Arg Pro Arg Leu Pro Val
210 215 220

Ser Trp Ser Phe Arg Thr Ser Ile Val Ser Asp Leu Thr Gly Ser Gln
225 230 235 240

Gln Arg Lys Arg Lys Phe Pro Ser Glu Ser Arg Pro Asn Val Val Lys
245 250 255

Pro Ser Val Leu Pro Ser Thr Ser Arg
260 265

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 552 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: Lelystad
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

ATG GCT GCG GCC ACT CTT TTC CTG GCT GGT GCT CAA CAT ATC ATG Met Ala Ala Ala Thr Leu Phe Phe Leu Ala Gly Ala Gln His Ile Met	48
1 5 10 15	
GTT TCT GAG GCG TTC GCC TGT AAG CCC TGT TTC TCG ACG CAT CTA TCA Val Ser Glu Ala Phe Ala Cys Lys Pro Cys Phe Ser Thr His Leu Ser	96
20 25 30	
GAT ATT GAG ACC AAC ACG ACC GCG GCT GCC GGT TTC ATG GTC CTT CAG Asp Ile Glu Thr Asn Thr Ala Ala Gly Phe Met Val Leu Gln	144
35 40 45	
GAC ATC AAT TGT TTC CGA CCT CAC GGG GTC TCA GCA GCG CAA GAG AAA Asp Ile Asn Cys Phe Arg Pro His Gly Val Ser Ala Ala Gln Glu Lys	192
50 55 60	
ATT TCC TTC GGA AAG TCG TCC CAA TGT CGT GAA GCC GTC GGT ACT CCC Ile Ser Phe Gly Lys Ser Ser Gln Cys Arg Glu Ala Val Gly Thr Pro	240
65 70 75 80	
CAG TAC ATC ACG ATA ACG GCT AAC GTG ACC GAC GAA TCA TAC TTG TAC Gln Tyr Ile Thr Ile Thr Ala Asn Val Thr Asp Glu Ser Tyr Leu Tyr	288
85 90 95	
AAC GCG GAC CTG CTG ATG CTT TCT GCG TGC CTT TTC TAC GCC TCA GAA Asn Ala Asp Leu Leu Met Leu Ser Ala Cys Leu Phe Tyr Ala Ser Glu	336
100 105 110	
ATG AGC GAG AAA GGC TTC AAA GTC ATC TTT GGG AAT GTC TCT GGC GTT Met Ser Glu Lys Gly Phe Lys Val Ile Phe Gly Asn Val Ser Gly Val	384
115 120 125	
GTT TCT GCT TGT GTC AAT TTC ACA GAT TAT GTG GCC CAT GTG ACC CAA Val Ser Ala Cys Val Asn Phe Thr Asp Tyr Val Ala His Val Thr Gln	432
130 135 140	
CAT ACC CAG CAG CAT CAT CTG GTA ATT GAT CAC ATT CGG TTG CTG CAT His Thr Gln Gln His His Leu Val Ile Asp His Ile Arg Leu Leu His	480
145 150 155 160	
TTC CTG ACA CCA TCT GCA ATG AGG TGG GCT ACA ACC ATT GCT TGT TTG Phe Leu Thr Pro Ser Ala Met Arg Trp Ala Thr Thr Ile Ala Cys Leu	528
165 170 175	
TTC GCC ATT CTC TTG GCA ATA TGA Phe Ala Ile Leu Leu Ala Ile	552
180	

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 183 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Met Ala Ala Ala Thr Leu Phe Phe Leu Ala Gly Ala Gln His Ile Met
1 5 10 15

Val Ser Glu Ala Phe Ala Cys Lys Pro Cys Phe Ser Thr His Leu Ser
20 25 30

Asp Ile Glu Thr Asn Thr Thr Ala Ala Ala Gly Phe Met Val Leu Gln
35 40 45

Asp Ile Asn Cys Phe Arg Pro His Gly Val Ser Ala Ala Gln Glu Lys
50 55 60

Ile Ser Phe Gly Lys Ser Ser Gln Cys Arg Glu Ala Val Gly Thr Pro
65 70 75 80

Gln Tyr Ile Thr Ile Thr Ala Asn Val Thr Asp Glu Ser Tyr Leu Tyr
85 90 95

Asn Ala Asp Leu Leu Met Leu Ser Ala Cys Leu Phe Tyr Ala Ser Glu
100 105 110

Met Ser Glu Lys Gly Phe Lys Val Ile Phe Gly Asn Val Ser Gly Val
115 120 125

Val Ser Ala Cys Val Asn Phe Thr Asp Tyr Val Ala His Val Thr Gln
130 135 140

His Thr Gln Gln His His Leu Val Ile Asp His Ile Arg Leu Leu His
145 150 155 160

Phe Leu Thr Pro Ser Ala Met Arg Trp Ala Thr Thr Ile Ala Cys Leu
165 170 175

Phe Ala Ile Leu Leu Ala Ile
180